



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 179670

TO: Satayanarayana Gudibande
Location: REM/3C04/3C18
Art Unit: 1654
Wednesday, February 15, 2006
Case Serial Number: 10/602394

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1a69
Phone: 571-272-2518

BOB
barbara.obryen@uspto.gov

Search Notes

This Page Blank (uspto)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2006, 20:01:37 ; Search time 116 Seconds
(without alignments)
37.877 Million cell updates/sec

Title: WRF

Perfect score: 58

Sequence:  ydwrfnafxy.103

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: geneseqp1980s.*
- 2: geneseqp1990s.*
- 3: geneseqp2000s.*
- 4: geneseqp2001s.*
- 5: geneseqp2002s.*
- 6: geneseqp2003as.*
- 7: geneseqp2003bs.*
- 8: geneseqp2004s.*
- 9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	98.3	10	9	ADW04630 Human AGR
2	57	98.3	10	9	ADW04629 Human AGR
3	46	79.3	2133	8	ADP25432 Plasmodiu
4	43	74.1	484	8	ADx80139 Plant ful
5	42	72.4	10	9	ADW04632 Human AGR
6	42	72.4	10	9	ADW04631 Human AGR
7	40	69.0	9	8	ADP25709 Plasmodiu
8	40	69.0	1804	2	ADH56613 Deduced p
9	40	69.0	1856	2	AAV21801 B. subtil
10	40	69.0	1856	3	AAy83269 Polypepti
11	39	67.2	666	4	ABx58019 Drosophil
12	39	67.2	1006	4	ABb70749 Drosophil
13	39	67.2	1364	3	AAAB42843 Human ORF
14	39	67.2	1365	9	ADY19343 PRO polyp
15	39	67.2	1368	8	ADL82927 Human PRO
16	39	67.2	1368	9	ADY18160 PRO polyp
17	39	67.2	1368	9	ADY17490 PRO polyp
18	39	67.2	1368	9	AEb86622 Human med
19	39	67.2	1439	4	ABB60094 Drosophil
20	38	65.5	315	7	ABO62364 Klebsiell
21	38	65.5	400	8	ADh52878 Bovine ap
22	37	63.8	135	8	ADk46463 Streptoco
23	37	63.8	152	8	ADR96377 Novel S.
24	37	63.8	152	9	AEA60247 Streptoco

25	37	63.8	233	6	ABU02359 S. pneumo
26	37	63.8	409	8	ADN26924 Bacterial
27	37	63.8	440	6	ABu20398 Protein e
28	37	63.8	618	9	ABM91016 M. xanthu
29	37	63.8	643	8	ADS27839 Bacterial
30	36.5	62.9	763	9	ABb48788 Pichia pa
31	36	62.1	184	8	ADx69103 Plant ful
32	36	62.1	191	6	ABM69582 Photorhab
33	36	62.1	212	8	ADx67448 Plant ful
34	36	62.1	276	8	ADv89584 Streptoco
35	36	62.1	276	8	ADv82391 Streptoco
36	36	62.1	276	8	ADv80837 Streptoco
37	36	62.1	498	7	ABO65670 Klebsiell
38	36	62.1	499	8	ADN17381 Bacterial
39	36	62.1	543	4	ABB63767 Drosophil
40	36	62.1	566	2	AAr13228 Endogluca
41	36	62.1	1062	8	ADP25429 Plasmodiu
42	35	60.3	9	7	ADW32693 HLA bindi
43	35	60.3	9	8	ADP80034 Human HLA
44	35	60.3	10	9	ADW04628 Human AGR
45	35	60.3	17	9	ADW04636 Human AGR

ALIGNMENTS

RESULT 1

ADW04630

ID ADW04630 standard; peptide; 10 AA.

XX AC ADW04630;

DT 10-MAR-2005 (first entry)

XX DE Human AGRP/MCR agonist chimeric cyclic peptide #4.

XX KW protein engineering; melanocortin receptor; AGRP; agouti related protein; obesity; gene therapy; anorectic; cyclic; melanocortin agonist.

XX OS Homo sapiens.

XX OS Chimeric.

XX OS Unidentified.

XX FH Key Location/Qualifiers

FT Misc-difference 2 /note= "This residue forms a lactam bridge with Dpr at position 9"

FT FT Misc-difference 5

FT FT Misc-difference 9 /note= "D-form residue"

FT FT Misc-difference 9 /note= "2,3-Diaminopropionic acid (Dpr) residue forms a lactam bridge with Asp at position 2"

FT FT US2004260063-A1.

XX 23-DEC-2004.

XX 23-JUN-2003; 2003US-00602394.

XX 23-JUN-2003; 2003US-00602394.

XX (HASK/) HASKELL-LUEVANO C.

XX Haskell-Luevano C;

XX WPI; 2005-030733/03.

XX New chimeric peptides and templates based upon melanocortin agonist peptides and agouti related protein antagonist peptide, useful for treating or preventing conditions modulated by melanocortin receptors, such as obesity.

XX Claim 2; SEQ ID NO 5; 15pp; English.

XX CC The present invention relates to a chimeric peptide that is biologically
CC active at melanocortin receptors (MCR) comprising an agouti (ASP) related
CC protein (AGRP) template and melanocortin agonist-based bioactive
CC determinant sequences which have been substituted for the analogous
CC template sequences. The invention is useful for treating or preventing
CC various diseases and conditions modulated by melanocortin receptors, such
CC as obesity and in gene therapy. The present sequence is the human
CC AGRP/MCR agonist chimeric cyclic peptide.

XX QY Sequence 10 AA;

Query Match 98.3%; Score 57; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YDWRFNAPXY 10
Db 1 YDWRFNAPXY 10
|||||

RESULT 2
ADM04629
ID ADM04629 standard; peptide; 10 AA.
XX AC ADM04629;
XX DT 10-MAR-2005 (first entry)
XX DE Human AGRP/MCR agonist chimeric cyclic peptide #3.
XX KW protein engineering; melanocortin receptor; AGRP; agouti related protein;
XX KW obesity; gene therapy; anorectic; cyclic; melanocortin agonist.
XX OS Homo sapiens.
XX OS Chimeric.
XX OS Unidentified.

Key Location/Qualifiers
FT Misc-difference 2 /note= "This residue forms a lactam bridge with Dpr at
FT position 9"
FT Misc-difference 9 /note= "2,3-Diaminopropionic acid (Dpr) residue forms a
FT lactam bridge with Asp at position 2"
XX US2004260063-A1.
XX PD 23-DEC-2004.
XX 23-JUN-2003; 2003US-00602394.
XX 23-JUN-2003; 2003US-00602394.
XX (HASK/) HASKELL-LUEVANO C.
XX PI Haskell-Luevano C;
XX DR WPI; 2005-030733/03.
XX New chimeric peptides and templates based upon melanocortin agonist
FT peptides and agouti related protein antagonist peptide, useful for
FT treating or preventing conditions modulated by melanocortin receptors,
FT such as obesity.

XX PS Claim 2; SEQ ID NO 4; 15pp; English.
XX CC The present invention relates to a chimeric peptide that is biologically
CC active at melanocortin receptors (MCR) comprising an agouti (ASP) related
CC protein (AGRP) template and melanocortin agonist-based bioactive
CC determinant sequences which have been substituted for the analogous
CC template sequences. The invention is useful for treating or preventing
CC various diseases and conditions modulated by melanocortin receptors, such

XX CC as obesity and in gene therapy. The present sequence is the human
CC AGRP/MCR agonist chimeric cyclic peptide.

XX QY Sequence 10 AA;

Query Match 98.3%; Score 57; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YDWRFNAPXY 10
Db 1 YDWRFNAPXY 10
|||||

RESULT 3
ADP25432
ID ADP25432 standard; protein; 2133 AA.
XX AC ADP25432;
XX DT 09-SEP-2004 (first entry)
XX DE Plasmodium falciparum antigen amino acid sequence SEQ ID NO:9.
XX KW Plasmodium falciparum; malaria parasite; antigen; malaria; immunogenic;
XX KW immune response; cytostatic; anti-HIV; virucide; hepatotropic;
XX KW antibacterial; vaccine; cancer; infectious disease; AIDS; hepatitis;
XX KW bacterial infection.
XX OS Plasmodium falciparum.
XX PN WO2004053086-A2.
XX PD 24-JUN-2004.
XX 08-DEC-2003; 2003WO-US038966.
XX 06-DEC-2002; 2002US-0431494P.
XX (EPIM-) EPIMMUNE INC.
XX (USNA) US SEC OF NAVY.
XX PI Sette A, Doolan DL, Carucci DJ, Sidney J, Southwood S;
XX WPI; 2004-468856/44.
XX New isolated and/or purified Plasmodium falciparum polynucleotide
FT sequences, useful in inducing an immune response for preventing and/or
FT treating cancer and infectious diseases, such as AIDS, hepatitis, and
FT bacterial infections.

XX PS Claim 22; SEQ ID NO 9; 253pp; English.
XX CC The present invention describes an isolated and/or purified Plasmodium
CC falciparum (malaria parasite) antigen polynucleotide sequence, encoding
CC an immunogenic peptide. Also described: (1) a primer or detection probe
CC for hybridisation with a target sequence or the amplicon generated from a
CC target sequence comprising a sequence of at least 8-30, 35, 40, 45, 50,
CC 55, 60, 65, 70, 75, 80, 85, 90, 95 or 100 consecutive nucleotides of any
CC of the polynucleotide sequences as described above; (2) a DNA chip
CC comprising any of the polynucleotide sequences described above; (3) a
CC vector comprising a promoter operably linked to any of the nucleic acid
CC sequences described above; (4) a host cell transformed by the vector of
CC (3) or the polynucleotide described above; (5) a composition comprising a
CC carrier and the polynucleotide described above; (6) a method of inducing
CC an immune response in an individual comprising the administration of the
CC composition of (5) to induce an immune response; (7) an isolated
CC polypeptide comprising any of the amino acid sequences as encoded by the
CC polynucleotide described above; (8) a composition comprising a carrier
CC and the polypeptide of (7); (9) a method of detecting P. falciparum in
CC biological samples, comprising contacting a biological sample with the
CC isolated polynucleotide and detecting the hybridisation of the isolated
CC polynucleotides with nucleic acids contained in the sample; (10) a method

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2006, 20:14:30 ; Search time 30.6667 Seconds
(without alignments)
26.959 Million cell updates/sec

Title: WRF

Perfect score: 58

Sequence: 1'YDWRFNAP 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA.*

- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCITUS COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	67.2	220	2	US-09-270-767-45997 Sequence 45997, A
2	38	65.5	98	2	US-09-270-767-36635 Sequence 36635, A
3	38	65.5	98	2	US-09-270-767-51852 Sequence 51852, A
4	38	65.5	315	2	US-09-489-039A-8881 Sequence 8881, Ap
5	37	63.8	135	2	US-09-583-110-2978 Sequence 2978, Ap
6	37	63.8	152	2	US-09-107-433-5012 Sequence 5012, Ap
7	37	63.8	618	2	US-09-902-540-10215 Sequence 10215, A
8	36	62.1	498	2	US-09-489-039A-12187 Sequence 12187, A
9	36	62.1	566	2	US-07-862-588B-4 Sequence 4, Appl
10	35	60.3	277	2	US-09-248-796A-15054 Sequence 15054, A
11	35	60.3	280	2	US-09-252-991A-16878 Sequence 16878, A
12	35	60.3	291	2	US-09-248-796A-16362 Sequence 16362, A
13	35	60.3	334	2	US-09-248-796A-16366 Sequence 16366, A
14	35	60.3	681	2	US-09-248-796A-16367 Sequence 16367, A
15	35	60.3	769	2	US-09-248-796A-16368 Sequence 16368, A
16	35	60.3	1476	2	US-09-817-514A-4 Sequence 4, Appl
17	35	60.3	1481	2	US-09-251-645-14 Sequence 14, Appl
18	34	58.6	62	2	US-09-134-001C-4031 Sequence 4031, Ap
19	34	58.6	144	2	US-09-155-036-12 Sequence 12, Appl
20	34	58.6	144	2	US-09-155-036-13 Sequence 13, Appl
21	34	58.6	144	2	US-09-155-036-14 Sequence 14, Appl
22	34	58.6	144	2	US-09-155-036-16 Sequence 16, Appl
23	34	58.6	144	2	US-09-866-307-12 Sequence 12, Appl
24	34	58.6	144	2	US-09-866-307-13 Sequence 13, Appl
25	34	58.6	144	2	US-09-866-307-14 Sequence 14, Appl
26	34	58.6	144	2	US-09-866-307-16 Sequence 16, Appl
27	34	58.6	145	2	US-09-155-036-15 Sequence 15, Appl

ALIGNMENTS

RESULT 1

US-09-270-767-45997
; Sequence 45997, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45997
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45997

Query Match 67.2%; Score 39; DB 2; Length 220;
Best Local Similarity 62.5%; Pred. No. 29;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 YDWRFNAP 8
DB 99 HDWRFNVP 106
:|:|:|

RESULT 2

US-09-270-767-36635
; Sequence 36635, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36635
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-36635
Query Match 65.5%; Score 38; DB 2; Length 98;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      2 DWRNAP 8
      ||| |||
Db      3 DWRLNAP 9

RESULT 3
US-09-270-767-51852
; Sequence 51852, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51852
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-51852

Query Match      65.5%; Score 38; DB 2; Length 98;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 DWRNAP 8
      ||| |||
Db      3 DWRLNAP 9

RESULT 4
US-09-489-039A-8881
; Sequence 8881, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489.039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8881
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8881

Query Match      65.5%; Score 38; DB 2; Length 315;
Best Local Similarity 85.7%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 YDWRNFA 7
      |||||
Db      232 YHWRNFA 238

RESULT 5
US-09-583-110-2978
; Sequence 2978, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583.110
; CURRENT FILING DATE: 2000-05-26
```

```
; PRIOR APPLICATION NUMBER: US 09/107.433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085.131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051.553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 2978
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-2978

Query Match      63.8%; Score 37; DB 2; Length 135;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1 YDWRNAP 10
      ||||: ||
Db      64 YDMKIVIFRY 73

RESULT 6
US-09-107-433-5012
; Sequence 5012, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION NUMBER: US/09/107.433
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5012:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...152
; SEQUENCE DESCRIPTION: SEQ ID NO: 5012:
US-09-107-433-5012
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2006, 20:15:26 ; Search time 127 seconds
(without alignments)
32.900 Million cell updates/sec

Title: WRF

Perfect score: 58

Sequence: ϵ_i ydwrfnafxy 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	74.1	484	US-10-425-114-49505	Sequence 49505, A
2	43	74.1	728	US-10-424-599-189465	Sequence 189465, A
3	42	72.4	89	US-10-425-115-197701	Sequence 197701, A
4	41	70.7	1114	US-10-437-963-178103	Sequence 178103, A
5	40	69.0	1769	US-10-361-522-3	Sequence 3, Appli
6	39	67.2	84	US-10-425-115-295441	Sequence 295441, A
7	39	67.2	666	US-11-097-143-849	Sequence 849, App
8	39	67.2	1006	US-11-097-143-39039	Sequence 39039, A
9	39	67.2	1368	US-10-405-387-2	Sequence 2, Appli
10	39	67.2	1439	US-11-097-143-7074	Sequence 7074, Ap
11	38	65.5	126	US-10-437-963-200586	Sequence 200586, A
12	38	65.5	127	US-10-437-963-104836	Sequence 104836, A
13	38	65.5	287	US-10-437-963-132229	Sequence 163229, A
14	38	65.5	459	US-10-437-963-118885	Sequence 118885, A
15	38	65.5	550	US-10-437-963-161824	Sequence 161824, A
16	38	65.5	599	US-10-437-963-126846	Sequence 126846, A
17	38	65.5	604	US-10-437-963-150085	Sequence 150085, A
18	38	65.5	788	US-10-437-963-204446	Sequence 204446, A
19	38	65.5	1133	US-10-437-963-143474	Sequence 143474, A
20	38	65.5	1309	US-10-437-963-115740	Sequence 115740, A
21	38	65.5	1426	US-10-437-963-169077	Sequence 169077, A
22	38	65.5	1452	US-10-437-963-128047	Sequence 128047, A
23	38	65.5	1493	US-10-437-963-170048	Sequence 170048, A
24	38	65.5	1529	US-10-437-963-204169	Sequence 204169, A
25	38	65.5	1569	US-10-437-963-117837	Sequence 117837, A
26	38	65.5	1685	US-10-437-963-171019	Sequence 171019, A
27	38	65.5	1698	US-10-437-963-192546	Sequence 192546, A

28 38 65.5 1770 4 US-10-437-963-117838 Sequence 117838, A

29 37 63.8 49 4 US-10-437-963-184166 Sequence 184166, A

30 37 63.8 152 5 US-10-617-320-5012 Sequence 5012, Ap

31 37 63.8 233 5 US-10-472-928-3874 Sequence 3874, Ap

32 37 63.8 361 4 US-10-437-963-199806 Sequence 199806, A

33 37 63.8 409 4 US-10-369-493-9577 Sequence 9577, Ap

34 37 63.8 440 4 US-10-282-122A-48322 Sequence 48322, A

35 37 63.8 643 4 US-10-369-493-16872 Sequence 16872, A

36 37 63.8 647 4 US-10-437-963-126808 Sequence 126808, A

37 37 63.8 742 4 US-10-424-599-227627 Sequence 227627, A

38 37 63.8 1012 4 US-10-437-963-107191 Sequence 107191, A

39 37 63.8 1588 4 US-10-437-963-196997 Sequence 196997, A

40 37 63.8 1663 4 US-10-437-963-143452 Sequence 143452, A

41 36 62.1 75 4 US-10-425-115-278415 Sequence 278415, A

42 36 62.1 184 4 US-10-425-114-39946 Sequence 39946, A

43 36 62.1 212 4 US-10-425-114-39291 Sequence 38291, A

44 36 62.1 308 4 US-10-424-599-283799 Sequence 283799, A

45 36 62.1 499 4 US-10-369-493-34 Sequence 34, Appl

ALIGNMENTS

RESULT 1

US-10-425-114-49505
; Sequence 49505, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 49505
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3051-077-E3_FLI.pep
US-10-425-114-49505

Query Match 74.1%; Score 43; DB 4; Length 484;
Best Local Similarity 80.0%; Pred. NO. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YDWRFNAPXY 10

DB 197 YDKRFNAPHY 206

RESULT 2

US-10-424-599-189465
; Sequence 189465, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 189465

```
; LENGTH: 728
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_142102C.1.pep
US-10-424-599-189465

Query Match      74.1%; Score 43; DB 4; Length 728;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YDWRFNAPFY 10
Db 441 YDKRFNAFY 450

RESULT 3
US-10-425-115-197701
; Sequence 197701, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425.115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 197701
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_111887C.1.pep
US-10-425-115-197701

Query Match      72.4%; Score 42; DB 4; Length 89;
Best Local Similarity 60.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YDWRFNAPFY 10
Db 47 YDWRMNVIAF 56

RESULT 4
US-10-437-963-178103
; Sequence 178103, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437.963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 178103
; LENGTH: 1114
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
```

```
; LOCATION: (1)..(1114)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_75692C.1.pep
US-10-437-963-178103

Query Match      70.7%; Score 41; DB 4; Length 1114;
Best Local Similarity 66.7%; Pred. No. 3.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 DWRFNAPFY 10
Db 696 DWRFDVFQY 704

RESULT 5
US-10-361-522-3
; Sequence 3, Application US/10361522
; Publication No. US20030232406A1
; GENERAL INFORMATION:
; APPLICANT: Perkins, John B
; APPLICANT: Sloma, Alan
; APPLICANT: Pero, Janice G
; APPLICANT: Hatch, Randolph T
; APPLICANT: Hermann, Theron
; APPLICANT: Erdenberg, Thomas
; TITLE OF INVENTION: BACTERIAL STRAINS WHICH OVERPRODUCE RIBOFLAVIN
; FILE REFERENCE: 13604 US6 (C38435/129129)
; CURRENT APPLICATION NUMBER: US/10/361.522
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US 09/306,615
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 1769
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-361-522-3

Query Match      69.0%; Score 40; DB 4; Length 1769;
Best Local Similarity 62.5%; Pred. No. 8.5e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YDWRFNAP 8
Db 1660 FDWQYNAP 1667

RESULT 6
US-10-425-115-295441
; Sequence 295441, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425.115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 295441
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_32522C.1.pep
US-10-425-115-295441

Query Match      67.2%; Score 39; DB 4; Length 84;
```


GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2006, 20:17:02 ; Search time 8 Seconds
(without alignments)
16.403 Million cell updates/sec

Title: WRF

Perfect score: 58

Sequence: %\$ydwrfnafxy.10%

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA New:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US03_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	67.2	1368	6	US-10-770-303-2
2	39	67.2	1368	7	US-11-185-372-2
3	35	60.3	1476	6	US-10-647-956A-4
4	33	56.9	270	7	US-11-098-686-10898
5	32	55.2	362	7	US-11-012-762-56
6	32	55.2	415	7	US-11-203-109-20
7	32	55.2	550	7	US-11-098-686-10696
8	32	55.2	1152	7	US-11-080-026-4
9	31	53.4	39	6	US-10-895-064-295
10	31	53.4	126	7	US-11-064-174-10
11	31	53.4	126	7	US-11-064-174-144
12	31	53.4	126	7	US-11-064-174-150
13	31	53.4	127	7	US-11-064-174-11
14	31	53.4	163	7	US-11-186-284-57
15	31	53.4	201	6	US-10-467-657-5880
16	31	53.4	316	7	US-11-152-811-4
17	31	53.4	317	7	US-11-052-554A-48
18	31	53.4	552	6	US-10-131-826A-332
19	31	53.4	809	6	US-10-467-657-1106
20	31	53.4	810	7	US-11-052-554A-245
21	30	51.7	123	6	US-10-910-463-8
22	30	51.7	193	7	US-11-108-163B-14
23	30	51.7	201	7	US-11-170-653-23
24	30	51.7	217	7	US-11-108-163B-13
25	30	51.7	220	7	US-11-108-163B-12

26 30 51.7 289 7 US-11-052-554A-75 Sequence 75, Appl
27 30 51.7 301 7 US-11-108-163B-11 Sequence 11, Appl
28 30 51.7 344 7 US-11-108-163B-10 Sequence 10, Appl
29 30 51.7 429 6 US-10-886-504-3 Sequence 3, Appl
30 30 51.7 429 6 US-10-886-504-4 Sequence 4, Appl
31 30 51.7 429 6 US-10-886-505-3 Sequence 3, Appl
32 30 51.7 429 6 US-10-886-505-4 Sequence 4, Appl
33 30 51.7 429 6 US-10-886-527-3 Sequence 3, Appl
34 30 51.7 429 6 US-10-886-527-4 Sequence 4, Appl
35 30 51.7 436 7 US-11-080-991-102 Sequence 102, Appl
36 30 51.7 527 6 US-10-886-504-9 Sequence 9, Appl
37 30 51.7 527 6 US-10-886-504-10 Sequence 10, Appl
38 30 51.7 527 6 US-10-886-505-9 Sequence 9, Appl
39 30 51.7 527 6 US-10-886-505-10 Sequence 10, Appl
40 30 51.7 527 6 US-10-886-527-9 Sequence 9, Appl
41 30 51.7 527 6 US-10-886-527-10 Sequence 10, Appl
42 30 51.7 787 6 US-10-517-939-54 Sequence 54, Appl
43 30 51.7 1194 7 US-11-039-686-10270 Sequence 10270, A
44 30 51.7 2710 7 US-11-051-453-41 Sequence 41, Appl
45 29.5 50.9 2233 6 US-10-873-528-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-10-770-303-2
; Sequence 2, Application US/10770303
; Publication No. US20050283007A1
; GENERAL INFORMATION:
; APPLICANT: Uesugi, Montonari
; APPLICANT: Asada, Shinichi
; TITLE OF INVENTION: Small Molecule Inhibitors of Her2 Expression
; FILE REFERENCE: HO-P02722US1/10213121
; CURRENT APPLICATION NUMBER: US/10/770,303
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: US 60/380,481
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 10/405,387
; PRIOR FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1368
; TYPE: PRT
; ORGANISM: Human
US-10-770-303-2

Query Match 67.2%; Score 39; DB 6; Length 1368;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 DWRENAF 8
Db 1091 DWRFNEF 1097

RESULT 2
US-11-185-372-2
; Sequence 2, Application US/11185372
; Publication No. US20050288327A1
; GENERAL INFORMATION:
; APPLICANT: Uesugi, Montonari
; APPLICANT: Asada, Shinichi
; TITLE OF INVENTION: Small Molecule Inhibitors of Her2 Expression
; FILE REFERENCE: HO-P02722US0/10213121
; CURRENT APPLICATION NUMBER: US/11/185,372
; CURRENT FILING DATE: 2005-07-20
; PRIOR APPLICATION NUMBER: US 60/380,481
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2

```
; LENGTH: 1368
; TYPE: PRT
; ORGANISM: Human
US-11-185-372-2

Query Match          67.2%; Score 39; DB 7; Length 1368;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DWRNFAF 8
Db 1091 DWRNEF 1097

RESULT 3
US-10-647-956A-4
; Sequence 4, Application US/10647956A
; Publication No. US20050251878A1
; GENERAL INFORMATION:
; APPLICANT: Iffrench-Constant, Richard
; APPLICANT: Bowen, David
; APPLICANT: Rocheleau, Thomas
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: 61645
; CURRENT APPLICATION NUMBER: US/10/647,956A
; CURRENT FILING DATE: 2003-08-26
; PRIOR FILING DATE: CURRENT FILING DATE: 2000-03-26
; PRIOR FILING DATE: CURRENT FILING DATE: 2000-03-26
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1476
; TYPE: PRT
; ORGANISM: Photorhabdus luminescens
US-10-647-956A-4

Query Match          60.3%; Score 35; DB 6; Length 1476;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YDWRFP 5
Db 1185 YDWRFP 1189

RESULT 4
US-11-098-686-10898
; Sequence 10898, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10898
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10898

Query Match          56.9%; Score 33; DB 7; Length 270;
Best Local Similarity 43.8%; Pred. No. 61;
```

```
Matches 7; Conservative 1; Mismatches 0; Indels 8; Gaps 1;

Qy 1 YDWRFP-----NAF 8
Db 83 YEWRFYTIDDDTVNAF 98

RESULT 5
US-11-012-762-56
; Sequence 56, Application US/11012762
; Publication No. US20050244815A1
; GENERAL INFORMATION:
; APPLICANT: Georgia State University Research Foundation, Inc.
; TITLE OF INVENTION: Compositions and Methods for Viral Resistance Genes
; FILE REFERENCE: GSU1.PCT
; CURRENT APPLICATION NUMBER: US/11/012,762
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: PCT/US03/19300
; PRIOR FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: US 60/390,046
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-012-762-56

Query Match          55.2%; Score 32; DB 7; Length 362;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YDWRFNAP 8
Db 158 YAWRYNKY 165

RESULT 6
US-11-205-109-20
; Sequence 20, Application US/11205109
; Publication No. US20050287641A1
; GENERAL INFORMATION:
; APPLICANT: Farnet, Chris
; APPLICANT: Zazopoulos, Emmanuel
; APPLICANT: Staffa, Alfredo
; TITLE OF INVENTION: GENE CLUSTER FOR RAMOPLANIN BIOSYNTHESIS
; FILE REFERENCE: 3002-2US
; CURRENT APPLICATION NUMBER: US/11/205,109
; CURRENT FILING DATE: 2005-08-17
; PRIOR APPLICATION NUMBER: US/09/976,059
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/239,924
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Actinoplanes sp.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1)
; OTHER INFORMATION: V represents a non-standard initiator codon. It is expected that
; OTHER INFORMATION: the biosynthesized protein will have a formylmethionine residue
; OTHER INFORMATION: at this position
US-11-205-109-20

Query Match          55.2%; Score 32; DB 7; Length 415;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WRFNA 7
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2006, 20:08:07 ; Search time 19 Seconds
(without alignments)
50.640 Million cell updates/sec

Title: WRF

Perfect score: 58

Sequence: i.ydwrfnafxy:1.0

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	72.4	561	2	G83913
2	38	65.5	363	2	G81445
3	37	63.8	233	2	B95218
4	37	63.8	233	2	A98082
5	37	63.8	643	2	C87412
6	37	63.8	651	2	PC1123
7	37	63.8	811	2	E97040
8	37	63.8	1436	2	A99115
9	36	62.1	125	2	E75624
10	36	62.1	327	2	D70346
11	36	62.1	499	2	C70345
12	36	62.1	566	2	JH0218
13	36	62.1	680	2	H90093
14	36	62.1	1483	2	E86143
15	35	60.3	163	2	E81971
16	35	60.3	191	2	A97074
17	35	60.3	206	2	D86772
18	35	60.3	263	2	E97189
19	35	60.3	268	2	B97189
20	35	60.3	337	2	F70960
21	35	60.3	345	2	T25580
22	35	60.3	371	2	AC0115
23	35	60.3	408	2	F83379
24	35	60.3	418	2	H97763
25	35	60.3	582	2	T05020
26	35	60.3	710	2	G82689
27	35	60.3	720	2	T02734
28	35	60.3	929	2	T28927
29	34.5	59.5	797	2	T39643

30	34	58.6	167	2	B71518
31	34	58.6	322	2	B84908
32	34	58.6	332	2	S40762
33	34	58.6	333	2	T02690
34	34	58.6	335	2	B71361
35	34	58.6	357	2	E75284
36	34	58.6	380	2	I38435
37	34	58.6	383	2	T50502
38	34	58.6	407	2	H87341
39	34	58.6	456	2	F47677
40	34	58.6	456	2	A50768
41	34	58.6	456	2	H85830
42	34	58.6	456	2	E90985
43	34	58.6	456	2	B55239
44	34	58.6	456	2	C90983
45	34	58.6	456	2	F85828

ALIGNMENTS

RESULT 1

G83913

hypothetical protein BH2111 [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C:Accession: G83913

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A:Reference number: AB3650; MUID:20512582; PMID:11058132

A:Accession: G83913

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-561 <STO>

A:Cross-references: UNIPROT:Q9XB24; UNIPARC:UPI00000C3DDA; GB:AP001514; GB:BA000004; NID

A:Experimental source: strain C-125

C:Genetics:

A:Gene: BH2111

Query Match 72.4%; Score 42; DB 2; Length 561;

Best Local Similarity 87.5%; Pred. No. 9.9;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YDWRFNAP 8

DB 227 YDWRFFAF 234

|||||

RESULT 2

G81445

hypothetical protein Cj0272 [imported] - Campylobacter jejuni (strain NCTC 11168)

C:Species: Campylobacter jejuni

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: G81445

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrel

Nature 403, 665-668, 2000

A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp

A:Reference number: AB1250; MUID:20150912; PMID:10688204

A:Accession: G81445

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-363 <PAR>

A:Cross-references: UNIPROT:Q9PIM3; UNIPARC:UPI00000C20B2; GB:AL139074; GB:AL111168; NID

A:Experimental source: serotype O2, strain NCTC 11168

C:Genetics:

A:Gene: Cj0272

C:Superfamily: Campylobacter jejuni hypothetical protein Cj0272

Query Match 65.5%; Score 38; DB 2; Length 363;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      3 WRFNAP 8
      |||||
Db     291 WRFNAP 296

RESULT 3
B95218
hypothetical protein SPI867 [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: B95218
R:Tectelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfle,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Lofthus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: B95218
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-233 <KUR>
A:Cross-references: UNIPROT:Q97NY4; UNIPARC:UPI0000051A08; GB:AE005672; PIDN:AAK75939.1;
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SPI867

      Query Match      63.8%; Score 37; DB 2; Length 233;
      Best Local Similarity 50.0%; Pred. No. 30;
      Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1 YDWRFNAPXY 10
      |||:: ||
Db     162 YDKYVIFRY 171

RESULT 4
A98082
UDPglucose 4-epimerase (EC 5.1.3.2) [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: A98082
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: A98082
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-233 <KUR>
A:Cross-references: UNIPROT:Q8DNJ6; UNIPARC:UPI000000E36D0; GB:AE007317; PIDN:AAI00486.1;
C:Genetics:
A:Gene: GalE-truncation
C:Keywords: isomerase

      Query Match      63.8%; Score 37; DB 2; Length 233;
      Best Local Similarity 50.0%; Pred. No. 30;
      Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1 YDWRFNAPXY 10
      |||:: ||
Db     162 YDKYVIFRY 171

RESULT 5
C87412
ABC transporter, HlyB/MsbA family CC1314 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

```

```

C:Accession: C87412
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: C87412
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-643 <STO>
A:Cross-references: UNIPROT:Q9A8N9; UNIPARC:UPI00000C7343; GB:AE005673; NID:gl3422655; P
C:Genetics:
A:Gene: CC1314

      Query Match      63.8%; Score 37; DB 2; Length 643;
      Best Local Similarity 85.7%; Pred. No. 85;
      Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 YDWRFNAP 7
      ||||| |
Db     216 YDWRFAA 222

RESULT 6
PC1123
hypothetical protein - bloodfluke planorb (fragment)
C:Species: Biomphalaria glabrata (bloodfluke planorb)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 17-Mar-1999
C:Accession: PC1123
R:Knight, M.; Miller, A.; Raghavan, N.; Richards, C.; Lewis, F.
Gene 118, 181-187, 1992
A:Title: Identification of a repetitive element in the snail Biomphalaria glabrata: Rela
A:Reference number: PC1123; MUID:92380502; PMID:1380940
A:Accession: PC1123
A:Molecule type: DNA
A:Residues: 1-651 <KNI>
A:Cross-references: UNIPARC:UPI000017BDA5; EMBL:X60372

      Query Match      63.8%; Score 37; DB 2; Length 651;
      Best Local Similarity 62.5%; Pred. No. 86;
      Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 YDWRFNAP 8
      ||||| ::|
Db     10 YDWRISSF 17

RESULT 7
E97040
phage related protein, YonO B. subtilis homolog [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: E97040
R:Nolling, J.; Berton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
; Baly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: E97040
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-811 <KUR>
A:Cross-references: UNIPROT:Q97JY3; UNIPARC:UPI000000CA0D9; GB:AE001437; PIDN:AAK79112.1;
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC1139

      Query Match      63.8%; Score 37; DB 2; Length 811;
      Best Local Similarity 62.5%; Pred. No. 1.1e+02;
      Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 YDWRFNAP 8

```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2006, 20:01:55 ; Search time 126.333 Seconds
(without alignments)
55.847 Million cell updates/sec

Title: WRF

Perfect score: 58

Sequence: 1 ydwrfnafxy 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	48	82.8	1686	Q7RSM1_PLAYO	Q7rsm1 plasmodium
2	46	79.3	1275	Q6BCJ7_TETTH	Q6bcj7 tetrahymena
3	46	79.3	2133	Q813V5_PLAF7	Q813v5 plasmodium
4	42	72.4	561	Q9KB24_BACHD	Q9kb24 bacillus ha
5	40	69.0	479	Q7PYW5_ANOGA	Q7pyw5 anopheles g
6	39	67.2	197	Q5WEN6_BACSK	Q5wen6 bacillus cl
7	39	67.2	367	Q7UMU6_RHOBA	Q7umu6 rhodospirill
8	39	67.2	397	Q4TDM8_TETNG	Q4tdw8 tetraodon n
9	39	67.2	485	Q5UQT3_MIMIV	Q5ugt3 mimivirus
10	39	67.2	520	Q8IRM5_DROME	Q8irm5 drosophila
11	39	67.2	523	Q9UIK4_DROME	Q9uik4 drosophila
12	39	67.2	540	Q8T5S7_DROME	Q8t5s7 drosophila
13	39	67.2	540	Q9VA63_DROSOPH	Q9va63 drosophila
14	39	67.2	541	Q4V4D0_DROSOPH	Q4v4d0 drosophila
15	39	67.2	590	Q5P0V3_AZOSE	Q5p0v3 azoarcus sp
16	39	67.2	617	Q5EB53_RAT	Q5eb59 rattus norv
17	39	67.2	691	Q9W318_DROSOPH	Q9w318 drosophila
18	39	67.2	1287	Q5TR75_ANOGA	Q5tr75 anopheles g
19	39	67.2	1311	Q7PNT3_ANOGA	Q7pnt3 anopheles g
20	39	67.2	1352	Q6BEG9_BRARE	Q6beg9 brachydanio
21	39	67.2	1359	Q6P9H6_HUMAN	Q6p9h6 homo sapien
22	39	67.2	1364	Q5JW73_HUMAN	Q5jw73 homo sapien
23	39	67.2	1365	Q5JW74_HUMAN	Q5jw74 homo sapien
24	39	67.2	1367	Q80YQ2_MOUSE	Q80yq2 mus musculu
25	39	67.2	1368	CRSP3_HUMAN	Q9ulk4 h cofactor
26	39	67.2	1369	Q6P423_XENLA	Q6p423 xenopus lae
27	39	67.2	1374	Q5JW72_HUMAN	Q5jw72 homo sapien
28	39	67.2	1378	Q5RIW8_BRARE	Q5riw8 brachydanio
29	39	67.2	1385	Q6ZPV7_MOUSE	Q6zpv7 mus musculu
30	39	67.2	1398	Q4SC38_TETNG	Q4sc38 tetraodon n
31	39	67.2	1439	Q9W1X7_DROME	Q9w1x7 drosophila

32 38 65.5 118 2 Q7YW22_9TRYP Q7yw22 trypanosoma
33 38 65.5 126 2 Q6Z669_ORYSA Q6z669 oryza sativ
34 38 65.5 162 2 Q7YVX1_9TRYP Q7yvxl1 trypanosoma
35 38 65.5 186 2 Q7YVZ1_9TRYP Q7yvzl1 trypanosoma
36 38 65.5 278 2 Q55LQ4_CRYNE Q55lq4 cryptococcu
37 38 65.5 278 2 Q5K919_CRYNE Q5k919 cryptococcu
38 38 65.5 284 2 Q51GQ0_ENTHI Q51gq0 entamoeba h
39 38 65.5 285 2 Q8R776_THETN Q8r776 thermoanaer
40 38 65.5 300 2 Q849X4_ECOLI Q849x4 escherichia
41 38 65.5 305 2 Q7PNP5_ANOGA Q7pnp5 anopheles g
42 38 65.5 363 2 Q5HWJ4_CAMJR Q5hwj4 campylobact
43 38 65.5 363 2 Q9PIM3_CAMJE Q9pim3 campylobact
44 38 65.5 385 2 Q8DIU9_SYNEL Q8diu9 synechococc
45 38 65.5 429 2 Q8AAZ7_BACTN Q8aaz7 bacteroides

ALIGNMENTS

RESULT 1

Q7RSM1_PLAYO PRELIMINARY; PRT; 1686 AA.
AC Q7RSM1;
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Phosphatidylinositol 3-kinase vps34-like.
GN Name=PY00334;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=2255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perte M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDAJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; AABL01000093; EAA22859.1; -; Genomic_DNA.
DR HSPF; P48736; IERY;
DR GO; GO:0004428; F:inositol or phosphatidylinositol kinase act. . . ; IEA.
DR InterPro; IPR000403; PI3/4_kinase_cat.
DR InterPro; IPR001263; PI3Ka.
DR Pfam; PF00454; PI3_P14_Kinase; 1.
DR Pfam; PF00613; PI3Ka; 1.
DR PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR PROSITE; PS00290; PI3_4_KINASE_3; 1.
KW Kinase; Nucleotide-binding.
SQ SEQUENCE 1686 AA; 200308 MW; D56F3FB5EBF016E3 CRC64;

Query Match 82.8%; Score 48; DB 2; Length 1686;

Best Local Similarity 70.0%; Pred. No. 17; Mismatches 2; Indels 0; Gaps 0;
Matches 7; Conservative 1;

OY 1 YDWRFNAPXY 10

Db 560 YDWMXENSPDY 569

RESULT 2

```

Q6BCJ7 TETH
ID Q6BCJ7 TETH PRELIMINARY; PRT; 1275 AA.
AC Q6BCJ7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Dicer-related RNase III protein Dclp.
GN Name=DCL1;
OS Tetrahymena thermophila.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Tetrahymenina; Tetrahymenidae; Tetrahymena.
OX NCBI_TaxID=5911;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=11598983; DOI=10.1101/gad.1265105;
RA Mochizuki K., Gorovsky M.A.;
RT "A Dicer-like protein in Tetrahymena has distinct functions in genome
RL rearrangement, chromosome segregation, and meiotic prophase.";
RL Genes Dev. 15:77-89(2005).
DR EMBL; AB182481; BAD34724.1; -; mRNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004519; F:endonuclease activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004525; F:ribonuclease III activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0006396; P:RNA processing; IEA.
DR InterPro; IPR000999; RNase III.
DR Pfam; PF00636; Ribonuclease_3; 2.
DR SMART; SM00535; RIBOC; 2.
DR PROSITE; PS0142; RNASE_3_2; 2.
SQ SEQUENCE 1275 AA; 150259 MW; 6C7470D27980D55B CRC64;

Query Match 79.3%; Score 46; DB 2; Length 1275;
Best Local Similarity 87.5%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YDWRFNAPF 8
Db 816 YDWRFNLF 823

RESULT 3
Q813V5 PLAF7
ID Q813V5 PLAF7 PRELIMINARY; PRT; 2133 AA.
AC Q813V5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Phosphatidylinositol 3-kinase, putative (EC 2.7.1.137).
GN Name=PF0765w;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22255708; PubMed=12368867; DOI=10.1038/nature01095;
RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
RA Feltwell T., Gobie A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,
RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
RA Seeger K., Sharp S., Smith R., Squares S., Stevens K.,
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Sulston J.E., Craig A., Newbold C., Barrall B.G.;
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
RL Nature 419:527-531(2002).

```

```

RN NUCLEOTIDE SEQUENCE.
RP Devlin K., Baker S., Davies P., Mungal K., Berriman M., Pain A.,
RA Hall N., Bowman S., Churcher C., Quail M., Barrall B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL929352; CAD51517.1; -; Genomic_DNA.
DR HSSP; P48736; 188Y.
DR GO; GO:0004428; F:inositol or phosphatidylinositol kinase act. .; IEA.
DR GO; GO:0016303; F:phosphatidylinositol 3-kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR000403; PI3/4_kinase_cat.
DR InterPro; IPR001263; PI3Ka.
DR Pfam; PF00454; PI3_P14_kinase; 1.
DR Pfam; PF00613; PI3Ka; 1.
DR SMART; SM00145; PI3Ka; 1.
DR SMART; SM00146; PI3KG; 1.
DR PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR PROSITE; PS02090; PI3_4_KINASE_3; 1.
KW Kinase; Nucleotide-binding; Transferase.
SQ SEQUENCE 2133 AA; 255921 MW; CF2E6C4B196FA4FC CRC64;

Query Match 79.3%; Score 46; DB 2; Length 2133;
Best Local Similarity 70.0%; Pred. No. 49;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YDWRFNAPFY 10
Db 774 YDWRFNPF 783

RESULT 4
Q9KB24 BACHD
ID Q9KB24 BACHD PRELIMINARY; PRT; 561 AA.
AC Q9KB24;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE BH2111 protein.
GN OrderedLocustNames=BH2111;
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; BA000004; BAB05830.1; -; Genomic_DNA.
DR PIR; G83913; G83913.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006059; SBP_bac_1.
DR Pfam; PF01547; SBP_bac_1; 1.
KW Complete proteome.
SQ SEQUENCE 561 AA; 64072 MW; BB76B1CA931D95A0 CRC64;

Query Match 72.4%; Score 42; DB 2; Length 561;
Best Local Similarity 87.5%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YDWRFNAPF 8
Db 227 YDWRFFAF 234

RESULT 5
Q7PYW5 ANOGA
ID Q7PYW5 ANOGA PRELIMINARY; PRT; 479 AA.

```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model
Run on: February 14, 2006, 20:01:37 ; Search time 116 Seconds
(without alignments)
37.877 Million cell updates/sec

Title: FRW
Perfect score: 58
Sequence: ~~1-ydfeawafxy~~10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	98.3	10	9	Adw04632 Human AGR
2	57	98.3	10	9	Adw04631 Human AGR
3	46.5	80.2	11	9	Adw04668 Human AGR
4	46.5	80.2	11	9	Adw04657 Human AGR
5	46.5	80.2	11	9	Adw04654 Human AGR
6	46.5	80.2	11	9	Adw04653 Human AGR
7	46.5	80.2	11	9	Adw04649 Human AGR
8	46.5	80.2	11	9	Adw04655 Human AGR
9	46.5	80.2	11	9	Adw04634 Human AGR
10	46.5	80.2	11	9	Adw04635 Human AGR
11	43.5	75.0	11	9	Adw04662 Human AGR
12	42	72.4	10	9	Adw04630 Human AGR
13	42	72.4	10	9	Adw04629 Human AGR
14	40.5	69.8	11	9	Adw04651 Human AGR
15	40	69.0	499	2	Aaw55660 H. pylori
16	40	69.0	528	2	Aaw55732 H. pylori
17	40	69.0	528	2	Aaw58295 H. pylori
18	40	69.0	528	2	Aay17167 H. pylori
19	40	69.0	528	5	Abb07348 H. pylori
20	40	69.0	528	5	Abb07349 H. pylori
21	40	69.0	528	5	Abb07347 H. pylori
22	40	69.0	528	6	Abu30791 Protein e
23	40	69.0	528	9	Abu91407 Microbial
24	40	69.0	881	6	Abu23568 Protein e

25	39.5	68.1	11	9	Adw04661	Adw04661 Human AGR
26	39.5	68.1	11	9	Adw04660	Adw04660 Human AGR
27	39.5	68.1	11	9	Adw04650	Adw04650 Human AGR
28	39.5	68.1	11	9	Adw04656	Adw04656 Human AGR
29	39.5	68.1	11	9	Adw04658	Adw04658 Human AGR
30	39.5	68.1	11	9	Adw04659	Adw04659 Human AGR
31	39	67.2	874	6	Abu48867	Abu48867 Protein e
32	38	65.5	310	4	AAU29393	AAU29393 Human G p
33	38	65.5	310	5	ABG60681	ABG60681 Novel G p
34	38	65.5	484	8	Adx80139	Adx80139 Plant ful
35	37	63.8	260	6	ABM69356	ABM69356 Phototrab
36	37	63.8	302	3	AAJ97213	AAJ97213 Campyloba
37	37	63.8	302	6	ABJ18492	ABJ18492 Campyloba
38	37	63.8	303	6	ABU26594	ABU26594 Protein e
39	37	63.8	309	3	AAAB18898	AAAB18898 A maize c
40	37	63.8	416	8	ADU05585	ADU05585 H. pylori
41	36	62.1	18	8	ADP47038	ADP47038 Murine he
42	36	62.1	128	8	ADP46948	ADP46948 Murine he
43	36	62.1	274	5	ABP64898	ABP64898 Human pro
44	36	62.1	274	7	ADD68864	ADD68864 Human ABC
45	36	62.1	323	2	AAAR35084	AAAR35084 (Pro)leuk

ALIGNMENTS

RESULT 1
ADW04632
ID ADW04632 standard; peptide; 10 AA.
XX AC ADW04632;
XX DT 10-MAR-2005 (first entry)
XX DE Human AGRP/MCR agonist chimeric cyclic peptide #6.
XX KW protein engineering; melanocortin receptor; AGRP; agouti related protein;
XX KW obesity; gene therapy; anorectic; cyclic; melanocortin agonist.
XX OS Homo sapiens.
XX OS Chimeric.
XX OS Unidentified.
XX FH Key Location/Qualifiers
FT Misc-difference 2 /note= "This residue forms a lactam bridge with Dpr at position 9"
FT Misc-difference 3 /note= "D-form residue"
FT Misc-difference 9 /note= "2,3-Diaminopropionic acid (Dpr) residue forms a lactam bridge with Asp at position 2"
FT Modified-site 10 /note= "C-terminal amide"
XX US2004260063-A1.
XX PD 23-DEC-2004.
XX PF 23-JUN-2003; 2003US-00602394.
XX PR 23-JUN-2003; 2003US-00602394.
XX PA (HASK/) HASKELL-LUEVANO C.
XX PI Haskell-Luevano C;
XX DR WPI; 2005-030733/03.
XX PT New chimeric peptides and templates based upon melanocortin agonist peptides and agouti related protein antagonist peptide, useful for treating or preventing conditions modulated by melanocortin receptors, such as obesity.
PT

XX PS Claim 2; SEQ ID NO 7; 15pp; English.

XX CC The present invention relates to a chimeric peptide that is biologically

XX CC active at melanocortin receptors (MCR) comprising an agouti (ASP) related

XX CC protein (AGRP) template and melanocortin agonist-based bioactive

XX CC determinant sequences which have been substituted for the analogous

XX CC template sequences. The invention is useful for treating or preventing

XX CC various diseases and conditions modulated by melanocortin receptors, such

XX CC as obesity and in gene therapy. The present sequence is the human

XX CC AGRP/MCR agonist chimeric cyclic peptide.

XX SQ Sequence 10 AA;

Query Match 98.3%; Score 57; DB 9; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.008;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YDFRWNAFY 10

Db 1 YDFRWNAFY 10

RESULT 2

ADW04631

ID ADW04631 standard; peptide; 10 AA.

XX AC ADW04631;

DT 10-MAR-2005 (first entry)

XX DE Human AGRP/MCR agonist chimeric cyclic peptide #5.

XX DE protein engineering; melanocortin receptor; AGRP; agouti related protein;

XX KW obesity; gene therapy; anorectic; cyclic; melanocortin agonist.

XX OS Homo sapiens.

XX OS Chimeric.

XX OS Unidentified.

XX FH Key Location/Qualifiers

XX FT Misc-difference 2 /note= "This residue forms a lactam bridge with Dpr at

XX FT position 9"

XX FT Misc-difference 9 /note= "2,3-Diaminopropionic acid (Dpr) residue forms a

XX FT lactam bridge with Asp at position 2"

XX PN US2004260063-A1.

XX PD 23-DEC-2004.

XX PF 23-JUN-2003; 2003US-00602394.

XX PR 23-JUN-2003; 2003US-00602394.

XX PA (HASK/) HASKELL-LUEVANO C.

XX PI Haskell-Luevano C;

XX DR WPI; 2005-030733/03.

XX XX New chimeric peptides and templates based upon melanocortin agonist

XX FT peptides and agouti related protein antagonist peptide, useful for

XX FT treating or preventing conditions modulated by melanocortin receptors,

XX FT such as obesity.

XX PS Claim 2; SEQ ID NO 6; 15pp; English.

XX CC The present invention relates to a chimeric peptide that is biologically

XX CC active at melanocortin receptors (MCR) comprising an agouti (ASP) related

XX CC protein (AGRP) template and melanocortin agonist-based bioactive

XX CC determinant sequences which have been substituted for the analogous

CC template sequences. The invention is useful for treating or preventing

CC various diseases and conditions modulated by melanocortin receptors, such

CC as obesity and in gene therapy. The present sequence is the human

CC AGRP/MCR agonist chimeric cyclic peptide.

XX SQ Sequence 10 AA;

Query Match 98.3%; Score 57; DB 9; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.008;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YDFRWNAFY 10

Db 1 YDFRWNAFY 10

RESULT 3

ADW04668

ID ADW04668 standard; peptide; 11 AA.

XX AC ADW04668;

XX DT 10-MAR-2005 (first entry)

XX DE Human AGRP/MCR agonist chimeric cyclic peptide #29.

XX DE protein engineering; melanocortin receptor; AGRP; agouti related protein;

XX KW obesity; gene therapy; anorectic; melanocortin agonist; cyclic.

XX OS Homo sapiens.

XX OS Chimeric.

XX OS Unidentified.

XX FH Key Location/Qualifiers

XX FT Misc-difference 2 /note= "This residue forms a lactam bridge with Dpr at

XX FT position 10"

XX FT Misc-difference 4 /label= D-form residue

XX FT Misc-difference 10 /note= "2,3-Diaminopropionic acid (Dpr) residue forms a

XX FT lactam bridge with Asp at position 2"

XX PN US2004260063-A1.

XX PD 23-DEC-2004.

XX PF 23-JUN-2003; 2003US-00602394.

XX PR 23-JUN-2003; 2003US-00602394.

XX PA (HASK/) HASKELL-LUEVANO C.

XX PI Haskell-Luevano C;

XX DR WPI; 2005-030733/03.

XX XX New chimeric peptides and templates based upon melanocortin agonist

XX FT peptides and agouti related protein antagonist peptide, useful for

XX FT treating or preventing conditions modulated by melanocortin receptors,

XX FT such as obesity.

XX PS Claim 5; SEQ ID NO 43; 15pp; English.

XX CC The present invention relates to a chimeric peptide that is biologically

XX CC active at melanocortin receptors (MCR) comprising an agouti (ASP) related

XX CC protein (AGRP) template and melanocortin agonist-based bioactive

XX CC determinant sequences which have been substituted for the analogous

XX CC template sequences. The invention is useful for treating or preventing

XX CC various diseases and conditions modulated by melanocortin receptors, such

XX CC as obesity and in gene therapy. The present sequence is the human

XX CC AGRP/MCR agonist chimeric cyclic peptide.

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2006, 20:14:30 ; Search time 30.6667 Seconds
(without alignments)
26.959 Million cell updates/sec

Title: FRW
Perfect score: 58
Sequence: 1 ydfrwnafxy 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5-COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6-COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H-COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCITUS-COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE-COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	63.8	303	2	US-09-495-406-17
2	37	63.8	303	2	US-09-816-028A-29
3	37	63.8	303	2	US-10-303-162-29
4	37	63.8	303	2	US-10-303-134-29
5	37	63.8	303	2	US-10-303-118-29
6	37	63.8	303	2	US-10-303-128-29
7	37	63.8	309	2	US-09-522-714-10
8	36	62.1	675	2	US-09-489-039A-9046
9	36	62.1	967	2	US-09-489-039A-8766
10	36	62.1	975	2	US-09-543-681A-5755
11	35	60.3	16	1	US-08-637-759B-344
12	35	60.3	16	2	US-08-871-355A-344
13	35	60.3	16	2	US-09-201-945-344
14	35	60.3	305	2	US-09-635-872A-3
15	35	60.3	305	2	US-09-636-077A-3
16	35	60.3	305	2	US-09-636-060C-3
17	35	60.3	305	2	US-09-636-552-3
18	35	60.3	305	2	US-09-636-596C-3
19	35	60.3	305	2	US-10-023-894-7
20	35	60.3	305	2	US-10-306-686-3
21	35	60.3	305	2	US-09-895-072-3
22	35	60.3	305	2	US-10-023-888-7
23	35	60.3	307	2	US-09-635-872A-9
24	35	60.3	307	2	US-09-636-077A-9
25	35	60.3	307	2	US-09-636-060C-9
26	35	60.3	307	2	US-09-986-552-9
27	35	60.3	307	2	US-09-636-596C-9

Sequence 12, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 12, Appl
Sequence 140, Appl
Sequence 4182, Ap
Sequence 58928, A
Sequence 40527, A
Sequence 55743, A
Sequence 7684, Ap
Sequence 17898, A
Sequence 10423, A
Sequence 1, Appl
Sequence 41679, A
Sequence 4305, Ap
Sequence 2350, Ap
Sequence 331, App
Sequence 8316, Ap

28 35 60.3 307 2 US-10-023-894-12
29 35 60.3 307 2 US-10-306-686-9
30 35 60.3 307 2 US-09-895-072-9
31 35 60.3 307 2 US-10-023-888-12
32 35 60.3 452 2 US-09-563-794B-140
33 35 60.3 961 2 US-09-328-352-4182
34 34 58.6 84 2 US-09-270-767-58928
35 34 58.6 86 2 US-09-270-767-40527
36 34 58.6 86 2 US-09-270-767-55743
37 34 58.6 190 2 US-09-543-681A-7684
38 34 58.6 206 2 US-09-248-796A-17898
39 34 58.6 208 2 US-09-489-039A-10423
40 34 58.6 208 2 US-09-393-171-1
41 34 58.6 226 2 US-09-270-767-41679
42 34 58.6 301 2 US-09-134-001C-4305
43 34 58.6 332 2 US-09-710-279-2350
44 34 58.6 390 2 US-09-634-238-331
45 34 58.6 390 2 US-09-489-039A-8316

ALIGNMENTS

RESULT 1

US-09-495-406-17
; Sequence 17, Application US/09495406
; Patent No. 6503744
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000110US
; CURRENT APPLICATION NUMBER: US/09/495,406
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
US-09-495-406-17

Query Match 63.8%; Score 37; DB 2; Length 303;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 1 YDFRWNAFY 10
| | | | |
Db 290 YQFKWKKFLY 299

RESULT 2

US-09-816-028A-29
; Sequence 29, Application US/09816028A
; Patent No. 669705
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/09/816,028A
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49

```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: Campylobacter glycosyltransferase B (CgtB) beta-1,3
; OTHER INFORMATION: galactosyltransferase from C. jejuni serotype O:2
; OTHER INFORMATION: (strain NCTC 11168)
US-09-816-028A-29

Query Match      63.8%; Score 37; DB 2; Length 303;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YDFRWNAFY 10
   |||||
Db 290 YQFKWKKFLY 299

RESULT 3
US-10-303-162-29
; Sequence 29, Application US/10303162
; Patent No. 6723545
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303.162
; CURRENT FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: Campylobacter glycosyltransferase B (CgtB) beta-1,3
; OTHER INFORMATION: galactosyltransferase from C. jejuni serotype O:2
; OTHER INFORMATION: (strain NCTC 11168)
US-10-303-162-29

Query Match      63.8%; Score 37; DB 2; Length 303;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YDFRWNAFY 10
   |||||
Db 290 YQFKWKKFLY 299

RESULT 4
US-10-303-134-29
; Sequence 29, Application US/10303134
; Patent No. 6825019
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303.134
; CURRENT FILING DATE: 2002-11-21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: Campylobacter glycosyltransferase B (CgtB) beta-1,3
; OTHER INFORMATION: galactosyltransferase from C. jejuni serotype O:2
; OTHER INFORMATION: (strain NCTC 11168)
US-10-303-134-29

Query Match      63.8%; Score 37; DB 2; Length 303;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YDFRWNAFY 10
   |||||
Db 290 YQFKWKKFLY 299

RESULT 5
US-10-303-118-29
; Sequence 29, Application US/10303118
; Patent No. 6905867
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303.118
; CURRENT FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: Campylobacter glycosyltransferase B (CgtB) beta-1,3
; OTHER INFORMATION: galactosyltransferase from C. jejuni serotype O:2
; OTHER INFORMATION: (strain NCTC 11168)
US-10-303-118-29

Query Match      63.8%; Score 37; DB 2; Length 303;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YDFRWNAFY 10
   |||||
Db 290 YQFKWKKFLY 299

RESULT 6
US-10-303-128-29
; Sequence 29, Application US/10303128
; Patent No. 6911337
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel

```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2006, 20:15:26 ; Search time 127 Seconds
(without alignments)
32.900 Million cell updates/sec

Title: FRW
Perfect score: 58
Sequence: 1 ydfrwnafxy 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /cgn2_6/ptodata/1/pubpaa/us07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/us08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/us09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/us10_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/us10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/us11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	69.0	77	US-10-335-977-4929	Sequence 4929, Ap
2	40	69.0	499	US-10-335-977-4932	Sequence 4932, Ap
3	40	69.0	528	US-09-881-752A-190	Sequence 190, App
4	40	69.0	528	US-10-282-122A-58715	Sequence 58715, A
5	40	69.0	528	US-10-335-977-4933	Sequence 4933, Ap
6	40	69.0	528	US-10-662-126-31	Sequence 31, Appl
7	40	69.0	881	US-10-282-122A-51492	Sequence 51492, A
8	39	67.2	874	US-10-282-122A-76791	Sequence 76791, A
9	38	65.5	310	US-09-811-284-142	Sequence 142, App
10	38	65.5	484	US-10-425-114-49505	Sequence 49505, A
11	38	65.5	728	US-10-424-599-189465	Sequence 189465, A
12	37	63.8	159	US-10-335-977-8565	Sequence 8565, Ap
13	37	63.8	205	US-10-424-599-145298	Sequence 145298, A
14	37	63.8	273	US-10-156-761-8617	Sequence 8617, Ap
15	37	63.8	303	US-09-816-028A-29	Sequence 29, Appl
16	37	63.8	303	US-10-303-161-29	Sequence 29, Appl
17	37	63.8	303	US-10-303-118-29	Sequence 29, Appl
18	37	63.8	303	US-10-303-128-29	Sequence 29, Appl
19	37	63.8	303	US-10-303-134-29	Sequence 29, Appl
20	37	63.8	303	US-10-303-162-29	Sequence 29, Appl
21	37	63.8	303	US-10-282-122A-54518	Sequence 54518, A
22	37	63.8	303	US-10-820-536-29	Sequence 29, Appl
23	37	63.8	303	US-10-845-408-29	Sequence 29, Appl
24	37	63.8	303	US-10-845-412-29	Sequence 29, Appl
25	37	63.8	303	US-10-846-219-29	Sequence 29, Appl
26	37	63.8	303	US-10-821-604-29	Sequence 29, Appl
27	37	63.8	303	US-10-847-983-29	Sequence 29, Appl

28	37	63.8	303	5	US-10-821-573-29	Sequence 29, Appl
29	37	63.8	303	5	US-10-850-807-29	Sequence 29, Appl
30	37	63.8	303	5	US-10-850-125-29	Sequence 29, Appl
31	37	63.8	303	5	US-10-830-825-29	Sequence 29, Appl
32	37	63.8	303	5	US-10-962-334-29	Sequence 29, Appl
33	37	63.8	303	5	US-10-830-997-29	Sequence 29, Appl
34	37	63.8	303	5	US-10-962-235-29	Sequence 29, Appl
35	37	63.8	303	5	US-10-961-882-29	Sequence 29, Appl
36	37	63.8	307	4	US-10-767-701-47078	Sequence 47078, A
37	37	63.8	309	4	US-10-304-928-10	Sequence 323462, A
38	37	63.8	313	4	US-10-425-115-323462	Sequence 11624, A
39	37	63.8	391	5	US-10-732-923-11624	Sequence 133410, A
40	37	63.8	567	4	US-10-437-963-133410	Sequence 133413, A
41	37	63.8	773	4	US-10-437-963-133413	Sequence 94, Appl
42	36	62.1	18	5	US-10-725-962-94	Sequence 4, Appl
43	36	62.1	128	5	US-10-725-962-4	Sequence 174643, A
44	36	62.1	135	4	US-10-424-599-174643	Sequence 59, Appl
45	36	62.1	254	6	US-11-090-847-59	

ALIGNMENTS

RESULT 1
US-10-335-977-4929
; Sequence 4929, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; City: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 4929:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...77
; SEQUENCE DESCRIPTION: SEQ ID NO: 4929:
US-10-335-977-4929

Query Match 69.0%; Score 40; DB 4; Length 77;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 0; Gaps 0;

QY 1 YDFRWNAFY 10
DB 12 YDWRNNAEY 21

RESULT 2

US-10-335-977-4932
; Sequence 4932, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: DOUGLAS SMITH et al
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-Dec-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 4932:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 499 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...499
; SEQUENCE DESCRIPTION: SEQ ID NO: 4932:

US-10-335-977-4932

Query Match 69.0%; Score 40; DB 4; Length 499;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YDFRWNAFY 10
DB 308 YDWRNNAEY 317

RESULT 3

US-09-881-752A-190
; Sequence 190, Application US/09881752A
; Patent No. US20020115078A1
; GENERAL INFORMATION:

; APPLICANT: Kleanthous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20020115078A1el Helicobacter Polypeptides in the
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 06132/041002
; CURRENT APPLICATION NUMBER: US/09/881,752A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 08/833,457
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 190
; LENGTH: 528
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-881-752A-190

Query Match 69.0%; Score 40; DB 3; Length 528;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YDFRWNAFY 10
DB 308 YDWRNNAEY 317

RESULT 4

US-10-282-122A-58715
; Sequence 58715, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2006, 20:17:02 ; Search time 8 Seconds
(without alignments)
16.403 Million cell updates/sec

Title: FRW
Perfect score: 58
Sequence: 1 ydfrwnafxy 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New.*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US03_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	69.0	528	7 US-11-052-554A-117	Sequence 117, Appl
2	36	62.1	454	7 US-11-024-959-458	Sequence 458, Appl
3	36	62.1	550	7 US-11-098-686-10696	Sequence 10696, A
4	34	58.6	332	6 US-10-793-626-2350	Sequence 2350, Ap
5	34	58.6	483	6 US-10-793-626-3132	Sequence 3132, Ap
6	33	56.9	294	7 US-11-098-686-10545	Sequence 10545, A
7	33	56.9	518	7 US-11-024-959-364	Sequence 364, Appl
8	33	56.9	529	7 US-11-037-243-62	Sequence 62, Appl
9	33	56.9	556	6 US-10-063-703-24	Sequence 24, Appl
10	33	56.9	556	6 US-11-102-240-24	Sequence 24, Appl
11	33	56.9	603	6 US-10-793-626-1684	Sequence 1684, Ap
12	33	56.9	625	7 US-11-055-822-522	Sequence 522, Appl
13	33	56.9	756	6 US-10-131-826A-392	Sequence 392, Appl
14	32.5	56.0	363	6 US-10-517-939-264	Sequence 264, Appl
15	32	55.2	93	6 US-10-467-657-5984	Sequence 5984, Ap
16	32	55.2	143	6 US-10-793-626-370	Sequence 370, Appl
17	32	55.2	269	6 US-10-467-657-2198	Sequence 2198, Ap
18	32	55.2	335	6 US-10-873-528-4	Sequence 4, Appl
19	32	55.2	396	6 US-11-032-773-941	Sequence 941, Appl
20	32	55.2	548	6 US-10-793-626-336	Sequence 326, Appl
21	32	55.2	599	7 US-11-165-141-33	Sequence 33, Appl
22	32	55.2	614	7 US-11-015-546A-20	Sequence 20, Appl
23	32	55.2	622	7 US-11-098-686-11191	Sequence 11191, A
24	32	55.2	622	7 US-10-994-820A-34	Sequence 34, Appl
25	32	55.2	763	7 US-11-013-247A-35	Sequence 35, Appl

26	32	55.2	1075	7 US-11-089-551A-23	Sequence 23, Appl
27	32	55.2	1237	7 US-11-052-554A-95	Sequence 95, Appl
28	32	55.2	1420	7 US-11-077-550-110	Sequence 110, Appl
29	31.5	54.3	693	7 US-11-098-686-11343	Sequence 11343, A
30	31	53.4	234	7 US-11-098-686-10686	Sequence 10686, A
31	31	53.4	338	7 US-11-207-626A-33	Sequence 33, Appl
32	31	53.4	341	7 US-11-207-626A-36	Sequence 36, Appl
33	31	53.4	343	7 US-11-207-626A-40	Sequence 40, Appl
34	31	53.4	393	7 US-11-207-626A-41	Sequence 41, Appl
35	31	53.4	410	7 US-11-055-822-6	Sequence 6, Appl
36	31	53.4	410	7 US-11-055-822-306	Sequence 306, Appl
37	31	53.4	410	7 US-11-055-822-332	Sequence 332, Appl
38	31	53.4	410	7 US-11-055-822-520	Sequence 520, Appl
39	31	53.4	456	7 US-11-055-822-4	Sequence 4, Appl
40	31	53.4	456	7 US-11-055-822-304	Sequence 304, Appl
41	31	53.4	456	7 US-11-055-822-330	Sequence 330, Appl
42	31	53.4	456	7 US-11-055-822-518	Sequence 518, Appl
43	31	53.4	520	7 US-11-094-917-44	Sequence 44, Appl
44	31	53.4	526	7 US-11-094-917-43	Sequence 43, Appl
45	31	53.4	882	7 US-11-098-686-10893	Sequence 10893, A

ALIGNMENTS

RESULT 1
US-11-052-554A-117
; Sequence 117, Application US/11052554A
; Publication No. US20050289866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 117
; LENGTH: 528
; TYPE: PRT
; ORGANISM: Helicobacter pylori J99
US-11-052-554A-117

Query Match 69.0%; Score 40; DB 7; Length 528;
Best Local Similarity 60.0%; Pred. No. 5.7;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YDFRWNAFX 10
Db 308 YDFRWNAFX 317

RESULT 2
US-11-024-959-458
; Sequence 458, Application US/11024959
; Publication No. US20060010516A1
; GENERAL INFORMATION:
; APPLICANT: FORSTER, RICHARD L.
; APPLICANT: CONNETT, SARAH JANE
; APPLICANT: EMERSON, SARAH JANE
; APPLICANT: GRIGOR, MURRAY ROBERT
; APPLICANT: HIGGINS, COLLEEN M.
; APPLICANT: LUND, STEVEN TROY
; APPLICANT: MAGUSIN, ANDREAS
; APPLICANT: KODRZYCKI, BOB
; TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
; FILE REFERENCE: 044463-0360
; CURRENT APPLICATION NUMBER: US/11/024,959

```

; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 60/533,036
; PRIOR FILING DATE: 2003-12-30
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 458
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Pinus radiata
US-11-024-959-458

Query Match      62.1%; Score 36; DB 7; Length 454;
Best Local Similarity 71.4%; Pred. No. 24;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 DFRWNAF 8
Db      394 DFWNSP 400

RESULT 3
US-11-098-686-10696
; Sequence 10696, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR FILING DATE: 2002-10-04
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10696
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10696

Query Match      62.1%; Score 36; DB 7; Length 550;
Best Local Similarity 70.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 YDFRWNAFY 10
Db      427 YDFRNNAYEY 436

RESULT 4
US-10-793-626-2350
; Sequence 2350, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2350
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence

US-10-793-626-2350
; Sequence 2350, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2350
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence

```

```

US-10-793-626-2350

Query Match      58.6%; Score 34; DB 6; Length 332;
Best Local Similarity 71.4%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 YDFRWNA 7
Db      131 HDFRWEA 137

RESULT 5
US-10-793-626-3132
; Sequence 3132, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3132
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-3132

Query Match      58.6%; Score 34; DB 6; Length 483;
Best Local Similarity 62.5%; Pred. No. 56;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      3 FRWNAFY 10
Db      332 FDNWSPKY 339

RESULT 6
US-11-098-686-10545
; Sequence 10545, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10545
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10545

Query Match      56.9%; Score 33; DB 7; Length 294;
Best Local Similarity 50.0%; Pred. No. 54;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 YDFRWNAF 8
Db      175 YDLQWNEY 182

```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2006, 20:08:07 ; Search time 19 Seconds
(without alignments)
50.640 Million cell updates/sec

Title: FRW
Perfect score: 58
Sequence: 1 ydfrwnafxy 10
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	69.0	528	2 F64580	hypothetical prote
2	40	69.0	528	2 F71931	outer membrane pro
3	40	69.0	881	2 G97195	valyl-tRNA synthet
4	39	67.2	205	2 C84334	hypothetical prote
5	39	67.2	874	2 E82913	valyl-tRNA synthet
6	38	65.5	395	2 D69312	molybdopterin oxid
7	38	65.5	955	2 F84972	valine-tRNA ligase
8	37	63.8	276	2 B71336	hypothetical prote
9	37	63.8	303	2 F81318	probable galactosy
10	37	63.8	416	2 C64590	hypothetical prote
11	37	63.8	416	2 D71367	hypothetical prote
12	37	63.8	426	2 D71367	conserved hypothet
13	37	63.8	660	2 E87391	TonB-dependent rec
14	36	62.1	300	2 B49238	gamma-hemolysin ga
15	36	62.1	323	2 JN0627	leukocidin chain F
16	36	62.1	323	2 J01530	leukocidin chain F
17	36	62.1	325	2 P00433	gamma-hemolysin co
18	36	62.1	325	2 B49234	leucocidin R, comp
19	36	62.1	325	2 JG7909	ATP-binding casset
20	36	62.1	531	2 T45865	hypothetical prote
21	36	62.1	664	2 T33379	hypothetical prote
22	36	62.1	951	1 SYECVT	valine-tRNA ligase
23	36	62.1	951	2 AC1061	valine-tRNA ligase
24	36	62.1	951	2 C81283	valine-tRNA synthet
25	36	62.1	951	2 E86124	valine-tRNA synthet
26	36	62.1	954	2 G64121	valine-tRNA ligase
27	36	62.1	956	2 B71250	valine-tRNA ligase
28	36	62.1	965	2 A80418	valine-tRNA ligase
29	36	62.1	994	2 B82843	valyl-tRNA synthet

ALIGNMENTS

RESULT 1

F64580
hypothetical protein HP0486 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: F64580
R:Tomb, J.F.; White, O.; Kervilange, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; son, J.D.; Kelley, J.M.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: F64580
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-528 <TOM>
A:Cross-references: UNIPROT:O25230; UNIPARC:UPI00000C084E; GB:AE000563; GB:AE000511; NID C:Superfamily: Helicobacter pylori hypothetical protein HP0209

Query Match 69.0%; Score 40; DB 2; Length 528;
Best Local Similarity 60.0%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YDFRWNAFYX 10
|||
Db 308 YDFRWNAEY 317

RESULT 2

F71931
outer membrane protein - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: Strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: F71931
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: F71931
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-528 <ARN>
A:Cross-references: UNIPROT:Q9ZLY7; UNIPARC:UPI00000D3626; GB:AE001478; GB:AE001439; NID C:Experimental source: strain J99
C:Genetics:
A:Gene: jhp0438
C:Superfamily: Helicobacter pylori hypothetical protein HP0209

Query Match 69.0%; Score 40; DB 2; Length 528;

```

Best Local Similarity 60.0%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YDFRWNAFY 10
Db 308 YDFRWNAEY 317
||| |||
||| |||

RESULT 3
G97195
valyl-tRNA synthetase [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: G97195
R;Nolling, J.; Bretton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325, PMID:21359325
A;Accession: G97195
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-881 <KUR>
A;Cross-references: UNIPROT:Q97GG8; UNIPARC:UPI000000CA4EA; GB:AE001437; PIDN:AAK80354.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
C;Superfamily: valine-tRNA ligase
A;Gene: CAC2399
Query Match 69.0%; Score 40; DB 2; Length 881;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YDFRWNAF 8
Db 641 YDFWMNEF 648
||| |||
||| |||

RESULT 4
C84334
hypothetical protein Vng183lh [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: C84334
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
; Leitthausner, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabc
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:1016950
A;Accession: C84334
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-205 <STO>
A;Cross-references: UNIPROT:Q9HP31; UNIPARC:UPI000006399E; GB:AE004437; NID:gl0581277; F
C;Genetics:
A;Gene: VNG1831H
Query Match 67.2%; Score 39; DB 2; Length 205;
Best Local Similarity 85.7%; Pred. No. 8.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YDFRWNA 7
Db 192 YDIRWNA 198
||| |||
||| |||

RESULT 5
E82913
valyl-tRNA synthetase UU267 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000

```

```

C;Accession: E82913
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A;Reference number: A82870
A;Accession: E82913
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-874 <GLA>
A;Cross-references: UNIPARC:UPI000013670D; GB:AE002123; GB:AF222894; NID:G6899229; PIDN:
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: vals; UU267
A;Genetic code: SGC3
C;Superfamily: valine-tRNA ligase
Query Match 67.2%; Score 39; DB 2; Length 874;
Best Local Similarity 75.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YDFRWNAF 8
Db 637 YDFIWNTF 644
||| |||
||| |||

RESULT 6
D69312
molybdopterin oxidoreductase, membrane subunit homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: D69312
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Goeyne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.;
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: D69312
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-395 <KLE>
A;Cross-references: UNIPROT:O29750; UNIPARC:UPI00000570A9; GB:AE001069; GB:AE000782; NID
Query Match 65.5%; Score 38; DB 2; Length 395;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 FRWNAEY 10
Db 127 FSWNAFLY 134
||| |||
||| |||

RESULT 7
F84972
valine-tRNA ligase (EC 6.1.1.9) [imported] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 03-Jun-2002
C;Accession: F84972
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
A;Reference number: A84930; MUID:20445173; PMID:10993077
A;Accession: F84972
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-955 <STO>
A;Cross-references: UNIPARC:UPI000005E561; GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: vals; BU366
C;Superfamily: valine-tRNA ligase

```


GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2006, 20:01:55 ; Search time 126.333 Seconds
(without alignments)
55.847 Million cell updates/sec

Title: FRW
Perfect score: 58
Sequence: 1 ydfrwnafxy 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	75.9	858	2	Q86IY5 dictyosteli
2	41	70.7	513	2	Q8XKG7 clostridium
3	41	70.7	944	2	Q4UQP3 xanthomonas
4	41	70.7	944	2	Q8PCR7 xanthomonas
5	41	70.7	944	2	Q8PGQ7 xanthomonas
6	41	70.7	980	2	Q5H4N5 xanthomonas
7	41	70.7	1263	2	Q50SH1 entamoeba h
8	40	69.0	293	2	Q7PMK7 anopheles g
9	40	69.0	469	2	Q744R2 mycoplasma
10	40	69.0	528	2	Q25230 helicobacte
11	40	69.0	528	2	Q8ZLX7 HELPU
12	40	69.0	880	2	Q891R5 CLOTE
13	40	69.0	881	2	Q97G98 CLOAB
14	40	69.0	937	2	Q4U920 theileria a
15	40	69.0	954	2	Q4N1R5 THEPA
16	39	67.2	205	2	Q8HP31 halobacteri
17	39	67.2	480	2	Q4I2V9 gibberella
18	39	67.2	560	2	Q4I0D0 GIBZE
19	39	67.2	590	2	Q5P0V3 azoarcus sp
20	39	67.2	874	1	SVU UREPA
21	39	67.2	960	1	SVU BUCAP
22	39	67.2	1572	2	Q4XV99 PLACH
23	39	67.2	1616	2	Q4YU25 PLABE
24	39	67.2	1623	2	Q7PDV5 PLAYO
25	39	67.2	1844	2	Q97287 PLAF7
26	38	65.5	309	2	Q6AFG1 LEIXX
27	38	65.5	383	2	Q6CH91 VARLIA
28	38	65.5	395	1	HNEB_ARCFU
29	38	65.5	556	2	Q5N445 AZOSE
30	38	65.5	627	2	Q5BD44 EMENI
31	38	65.5	703	2	Q4WC74 ASPFU

Q8eup6 mycoplasma
P57447 buchnera ap
Q4ugr2 theileria a
O7m558 brachydanio
Q7n246 photorhabdu
Q985r2 rhizobium l
Q82p55 streptomyce
P96089 thermoanaer
Q9jrq2 thermoanaer
Q9pnfs campylobact
Q4mj80 serratia pr
Q4tmj2 erythrobaet
Q9hjz2 thermoplasma

ALIGNMENTS

RESULT 1

Q86IY5 D1CDI
ID Q86IY5 D1CDI PRELIMINARY; PRT; 858 AA.
AC Q86IY5
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=DD80167886;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J.A.,
RA Bankier A.T., Dear P.H., Lehmann R., Baumgart C., Parra G.,
RA Abril J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A.,
RA Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL Nature 418:79-85(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhrouou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourlet T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Louissegh H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Ushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstein G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzner M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2005).
DR EMBL; AC116986; AAC01863.1; -; Genomic DNA.
DR EMBL; AAF101000027; EAL70063.1; -; Genomic DNA.
DR DictyBase; DDB0168226; JCV2V2_0_00892.
DR InterPro; IPR011020; HTTM.

```

DR SMART; SMO0752; HTTM; 1.
KW Hypothetical protein.
SQ SEQUENCE 858 AA; 98593 MW; 040A389DB900EC95 CRC64;

Query Match 75.9%; Score 44; DB 2; Length 858;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YDFRWNAPXY 10
   ||: ||| ||
DB 706 YDYSWQFAY 715

RESULT 2
ID Q8XKG7 CLOPE PRELIMINARY; PRT; 513 AA.
AC Q8XKG7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein CPE1429.
GN OrderedLocusNames=CPE1429;
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; BA000016; BAB81135.1; -; Genomic DNA.
DR GO; GO:0015969; P:guanosine tetraphosphate metabolism; IEA.
DR InterPro; IPR007685; RelA_Spot.
DR Pfam; PF04607; RelA_Spot; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 513 AA; 60477 MW; 159D0E05B4A0B1EA CRC64;

Query Match 70.7%; Score 41; DB 2; Length 513;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YDFRWNAP 8
   ||| ||| ||
DB 335 YDFHWNLF 342

RESULT 3
ID Q4UQP3 XANCP PRELIMINARY; PRT; 944 AA.
AC Q4UQP3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Valyl-tRNA synthetase.
GN ORFNames=XC3588;
OS Xanthomonas campestris pv. campestris str. 8004.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=314565;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=8004;
RA Qian W., Jia Y.-T., Ren S.-X., He Y.-Q., Feng J.-X., Lu L.-F.,
RA Sun Q.-H., Ying G., Tang D.-J., Wu W., Wang L.-F., Jiang B.-L.,
RA Zeng S.-Y., Gu W.-Y., Lu G., Rong L., Tian Y.-C., Yao Z.-J., Fu G.,
RA Chen B.-S., Fang R.-X., Qiang B.-Q., Chen Z., Zhao G.-P., Tang J.-L.,
RA He C.-Z.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

```

```

CC -!- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) = AMP + diphosphate
CC + L-valyl-tRNA(Val).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
DR EMBL; CP000050; AAY50630.1; -; Genomic_DNA.
DR InterPro; IPR002300; tRNA-synt_1a.
DR InterPro; IPR001412; tRNA-synt_I.
DR InterPro; IPR002303; tRNA-synt_val.
DR Pfam; PF00133; tRNA-synt_1; 1.
DR PRINTS; PR00986; TRNASYNTHAL.
DR TIGRFAMs; TIGR00422; vals; 1.
DR PROSITE; PS00178; AA tRNA LIGASE I; 1.
KW ATP-binding; Aminoacyl-tRNA synthetase; Ligase; Nucleotide-binding;
KW Protein biosynthesis.
SQ SEQUENCE 944 AA; 106095 MW; 73EA22380436B10D CRC64;

Query Match 70.7%; Score 41; DB 2; Length 944;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YDFRWNAP 8
   ||: ||| ||
DB 699 YEFANNAF 706

RESULT 4
ID Q8PCR7 XANCP PRELIMINARY; PRT; 944 AA.
AC Q8PCR7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Valyl-tRNA synthetase.
GN Names=vals;
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Uagiao R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,
RA Almeida N.F., Jr., Alves L.M.C., do Amaral A.M., Bertolini M.C.,
RA Ciapina L.E.A., Camarotte G., Cannavaro F., Cardoso J., Chambergo F.,
RA El-Dorri H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,
RA Ferro M.I.T., Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.P., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White P.F.,
RA Stubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
DR EMBL; AE012162; AAM39962.1; -; Genomic_DNA.
DR HSP; P96142; IIVS.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0004832; P:valine-tRNA ligase activity; IEA.
DR GO; GO:0006438; P:valyl-tRNA aminoacylation; IEA.
DR InterPro; IPR002300; tRNA-synt_1a.
DR InterPro; IPR001412; tRNA-synt_I.
DR InterPro; IPR002303; tRNA-synt_val.
DR Pfam; PF00133; tRNA-synt_1; 1.
DR PRINTS; PR00986; TRNASYNTHAL.
DR TIGRFAMs; TIGR00422; vals; 1.
DR PROSITE; PS00178; AA tRNA LIGASE I; 1.
KW Aminoacyl-tRNA synthetase; Complete proteome.

```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: February 14, 2006, 20:01:37 ; Search time 116 Seconds
(without alignments)
37.877 Million cell updates/sec
Title: HFRW
Perfect score: 60
Sequence: %k-ydhfrwafxy*10 \$
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : A_Geneseq_21:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48.5	80.8	11	9	Adw04668 Human AGR
2	48.5	80.8	11	9	Adw04657 Human AGR
3	48.5	80.8	11	9	Adw04634 Human AGR
4	48.5	80.8	11	9	Adw04635 Human AGR
5	45.5	75.8	11	9	Adw04662 Human AGR
6	42.5	70.8	11	9	Adw04651 Human AGR
7	41.5	69.2	11	9	Adw04660 Human AGR
8	41.5	69.2	11	9	Adw04658 Human AGR
9	41.5	69.2	11	9	Adw04659 Human AGR
10	41.5	67.5	11	9	Adw04650 Human AGR
11	40.5	66.7	8	4	ABB80033 Template
12	40	66.7	89	2	AAY23670 Human bet
13	40	66.7	424	8	Adn24572 Bacterial
14	40	66.7	431	8	Adq79875 T. thermo
15	40	66.7	431	8	Adq79873 T. thermo
16	40	66.7	431	8	Adq79877 T. thermo
17	40	66.7	431	8	Adq79881 Thermus s
18	40	66.7	431	8	Adq79700 Thermus t
19	40	66.7	431	8	Adq79706 Thermus t
20	40	66.7	431	8	Adq79698 Thermus t
21	40	66.7	431	8	Adq79702 Thermus f
22	40	66.7	431	8	Adq75571 Thb beta-
23	40	66.7	431	8	Adq75569 Tat beta-
24	40	66.7	431	8	Adq75571 Thb beta-

25	40	66.7	431	8	Adq75573 Tfi beta-
26	40	66.7	431	8	Adq75577 Tib10 bet
27	40	66.7	436	8	Adq79879 Thermus s
28	40	66.7	436	8	Adq79704 Thermus t
29	40	66.7	436	8	Adq75575 Tib2 beta
30	40	66.7	449	8	AdS30418 Bacterial
31	40	66.7	451	8	Adn21812 Bacterial
32	40	66.7	488	8	Adn25473 Bacterial
33	40	66.7	513	2	AAW42119 Coniferin
34	40	66.7	556	6	ABU21343 Protein e
35	39.5	65.8	11	9	Adw04654 Human AGR
36	39.5	65.8	11	9	Adw04655 Human AGR
37	39	65.0	6	3	AAAB11848 Alpha-MSH
38	39	65.0	7	3	AAAB11852 Alpha-MSH
39	39	65.0	8	3	AAAB11856 Alpha-MSH
40	38.5	64.2	11	9	Adw04656 Human AGR
41	38.5	64.2	11	9	Adw04653 Human AGR
42	38.5	64.2	11	9	Adw04649 Human AGR
43	38	63.3	161	6	ABM69386 PhotOrhab
44	38	63.3	395	2	AAY37052 Protein i
45	38	63.3	660	6	ABU27245 Protein e

ALIGNMENTS

RESULT 1
ADW04668
ID ADW04668 standard; peptide; 11 AA.
XX
AC ADW04668;
XX
DT 10-MAR-2005 (first entry)
XX
DE Human AGR\MCR agonist chimeric cyclic peptide #29.
XX
KW protein engineering; melanocortin receptor; AGRP; agouti related protein;
KW obesity; gene therapy; anorectic; melanocortin agonist; cyclic.
XX
OS Homo sapiens.
OS Chimeric.
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Misc-difference 2 /note= "This residue forms a lactam bridge with Dpr at position 10"
FT FT
FT Misc-difference 4 /label= D-form residue
FT FT
FT Misc-difference 10 /note= "2,3-Diaminopropionic acid (Dpr) residue forms a lactam bridge with Asp at position 2"
XX
PN US2004260063-A1.
XX
PD 23-DEC-2004.
XX
PF 23-JUN-2003; 2003US-00602394.
XX
PR 23-JUN-2003; 2003US-00602394.
XX
PA (HASK/) HASKELL-LUEVANO C.
XX
PI Haskell-Luevano C;
XX
DR WPI; 2005-030733/03.
XX
PT New chimeric peptides and templates based upon melanocortin agonist peptides and agouti related protein antagonist peptide, useful for treating or preventing conditions modulated by melanocortin receptors, such as obesity.
XX
PS Claim 5; SEQ ID NO 43; 15pp; English.

CC The present invention relates to a chimeric peptide that is biologically
 CC active at melanocortin receptors (MCR) comprising an agouti (ASP) related
 CC protein (AGRP) template and melanocortin agonist-based bioactive
 CC determinant sequences which have been substituted for the analogous
 CC template sequences. The invention is useful for treating or preventing
 CC various diseases and conditions modulated by melanocortin receptors, such
 CC as obesity and in gene therapy. The present sequence is the human
 CC AGRP/MCR agonist chimeric cyclic peptide.
 SQ Sequence 11 AA;

Query Match 80.8%; Score 48.5; DB 9; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.1;
 Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 YDHFWR-AEYX 10
 Db 1 YDHFWRNAFYX 11

RESULT 2
 ADW04657
 ID ADW04657 standard; peptide; 11 AA.
 AC ADW04657;
 XX
 DT 10-MAR-2005 (first entry)
 DE Human AGRP\MCR agonist chimeric cyclic peptide #18.
 XX
 KW protein engineering; melanocortin receptor; AGRP; agouti related protein;
 KW obesity; gene therapy; anorectic; melanocortin agonist; cyclic.
 XX
 OS Homo sapiens.
 OS Chimeric.
 OS Unidentified.

XX Key Location/Qualifiers
 FH Misc-difference 2 /note= "This residue forms a lactam bridge with Dpr at
 FT position 10"
 FT Modified-site 4 /note= "D-form residue, (pI)Dphe"
 FT Misc-difference 10 /note= "2,3-Diaminopropionic acid (Dpr) residue forms a
 FT lactam bridge with Asp at position 2"
 XX US2004260063-A1.
 XX 23-DEC-2004.
 XX 23-JUN-2003; 2003US-00602394.
 XX 23-JUN-2003; 2003US-00602394.
 XX (HASK/) HASKELL-LUEVANO C.
 XX Haskell-Luevano C;
 XX WPI; 2005-030733/03.
 XX New chimeric peptides and templates based upon melanocortin agonist
 FT peptides and agouti related protein antagonist peptide, useful for
 FT treating or preventing conditions modulated by melanocortin receptors,
 FT such as obesity.
 XX Claim 5; SEQ ID NO 32; 15pp; English.
 XX The present invention relates to a chimeric peptide that is biologically
 CC active at melanocortin receptors (MCR) comprising an agouti (ASP) related
 CC protein (AGRP) template and melanocortin agonist-based bioactive
 CC determinant sequences which have been substituted for the analogous

CC template sequences. The invention is useful for treating or preventing
 CC various diseases and conditions modulated by melanocortin receptors, such
 CC as obesity and in gene therapy. The present sequence is the human
 CC AGRP/MCR agonist chimeric cyclic peptide.
 SQ Sequence 11 AA;

Query Match 80.8%; Score 48.5; DB 9; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.1;
 Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 YDHFWR-AEYX 10
 Db 1 YDHFWRNAFYX 11

RESULT 3
 ADW04634
 ID ADW04634 standard; peptide; 11 AA.
 AC ADW04634;
 XX
 DT 10-MAR-2005 (first entry)
 DE Human AGRP\MCR agonist chimeric cyclic peptide #8.
 XX
 KW protein engineering; melanocortin receptor; AGRP; agouti related protein;
 KW obesity; gene therapy; anorectic; cyclic; melanocortin agonist.
 XX
 OS Homo sapiens.
 OS Chimeric.
 OS Unidentified.

XX Key Location/Qualifiers
 FH Misc-difference 2 /note= "This residue forms a lactam bridge with Dpr at
 FT position 10"
 FT Misc-difference 10 /note= "2,3-Diaminopropionic acid (Dpr) residue forms a
 FT lactam bridge with Asp at position 2"
 XX US2004260063-A1.
 XX 23-DEC-2004.
 XX 23-JUN-2003; 2003US-00602394.
 XX 23-JUN-2003; 2003US-00602394.
 XX (HASK/) HASKELL-LUEVANO C.
 XX Haskell-Luevano C;
 XX WPI; 2005-030733/03.
 XX New chimeric peptides and templates based upon melanocortin agonist
 FT peptides and agouti related protein antagonist peptide, useful for
 FT treating or preventing conditions modulated by melanocortin receptors,
 FT such as obesity.
 XX Claim 2; SEQ ID NO 9; 15pp; English.
 XX The present invention relates to a chimeric peptide that is biologically
 CC active at melanocortin receptors (MCR) comprising an agouti (ASP) related
 CC protein (AGRP) template and melanocortin agonist-based bioactive
 CC determinant sequences which have been substituted for the analogous
 CC template sequences. The invention is useful for treating or preventing
 CC various diseases and conditions modulated by melanocortin receptors, such
 CC as obesity and in gene therapy. The present sequence is the human
 CC AGRP/MCR agonist chimeric cyclic peptide.
 SQ Sequence 11 AA;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2006, 20:14:30 ; Search time 30.6667 Seconds
(without alignments)
26.959 Million cell updates/sec

Title: HFRW

Perfect score: 60

Sequence: <1 ydhrwafxy 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA.*
1: /cgn2_6/ptodata/1/iaa/5-COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6-COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H-COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PTUS-COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE-COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	66.7	89	2	US-09-217-228-29
2	40	66.7	513	1	US-09-122-230-7
3	38	63.3	662	2	US-09-198-452A-169
4	38	63.3	665	2	US-09-438-185A-151
5	37	61.7	14	1	US-08-480-190-176
6	37	61.7	14	1	US-08-488-379-176
7	37	61.7	14	2	US-08-475-399A-176
8	37	61.7	14	2	US-08-077-255A-176
9	37	61.7	14	4	PCT-US93-07545-176
10	37	61.7	396	2	US-08-860-656B-3
11	37	61.7	396	2	US-08-860-656B-4
12	37	61.7	441	2	US-08-914-375C-63
13	37	61.7	448	2	US-09-306-593-12
14	37	61.7	497	2	US-09-902-540-15207
15	37	61.7	1836	2	US-10-162-012-24
16	37	61.7	6	2	US-09-623-548A-34
17	36	60.0	6	2	US-09-657-276-34
18	36	60.0	6	2	US-08-345-902B-15
19	36	60.0	7	1	US-09-240-078-54
20	36	60.0	7	2	US-09-374-827-6
21	36	60.0	7	2	US-09-953-349-6
22	36	60.0	7	2	US-09-458-580-6
23	36	60.0	105	2	US-08-851-362D-30
24	36	60.0	136	2	US-09-621-976-3913
25	36	60.0	162	1	US-08-624-125-8
26	36	60.0	162	2	US-08-937-155-8
27	36	60.0			

28	36	60.0	162	2	US-09-323-998E-8
29	36	60.0	355	1	US-09-014-969-19
30	36	60.0	477	2	US-09-991-181-285
31	36	60.0	477	2	US-09-990-444-285
32	36	60.0	477	2	US-09-997-333-285
33	36	60.0	477	2	US-09-992-598-285
34	36	60.0	567	1	US-08-504-459-2
35	36	60.0	567	1	US-08-504-459-4
36	36	60.0	567	1	US-08-504-459-6
37	35	58.3	86	2	US-09-270-767-36243
38	35	58.3	86	2	US-09-270-767-51460
39	35	58.3	439	2	US-08-914-375C-67
40	35	58.3	609	2	US-09-257-525A-9
41	35	58.3	671	2	US-09-843-598-5
42	35	58.3	671	2	US-09-843-598-7
43	35	58.3	1024	2	US-09-562-737-88
44	35	58.3	3418	1	US-08-639-501-2
45	35	58.3	3418	1	US-08-603-753D-4

ALIGNMENTS

RESULT 1

US-09-217-228-29

; Sequence 29, Application US/09217228

; Patent No. 6323178

; GENERAL INFORMATION:

; APPLICANT: Butler, Jon P.

; APPLICANT: Hale, John E.

; APPLICANT: Heath Jr., William F.

; APPLICANT: Schoner, Brigitte E.

; APPLICANT: Heiman, Mark L.

; APPLICANT: Becker, Gerald W.

; APPLICANT: Varshavsky, Alexander D.

; TITLE OF INVENTION: Beta-lipotropin and Uses Thereof

; FILE REFERENCE: X-12139

; CURRENT APPLICATION NUMBER: US/09/217,228

; CURRENT FILING DATE: 1998-12-21

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 29

; LENGTH: 89

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Human analog

US-09-217-228-29

Query Match 66.7%; Score 40; DB 2; Length 89;

Best Local Similarity 100.0%; Pred. No. 7.4;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DHFRWA 7

Db 46 DHFRWA 51

RESULT 2

US-09-122-230-7

; Sequence 7, Application US/09122230A

; Patent No. 5973228

; GENERAL INFORMATION:

; APPLICANT: Carlson, et al.

; TITLE OF INVENTION: Coniferin Beta Glucosidase cDNA for Modifying Lignin

; FILE REFERENCE: 50532

; CURRENT APPLICATION NUMBER: US/09/122,230A

; CURRENT FILING DATE: 1998-07-23

; EARLIER APPLICATION NUMBER: U.S. 60/053,566

; EARLIER FILING DATE: 1997-07-24

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn Ver. 2.0

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2006, 20:15:26 ; Search time 127 Seconds
(without alignments)
32.900 Million cell updates/sec

Title: HFRW

Perfect score: 60

Sequence: 1-ydhrfwafxy 10 *

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA Main:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	75.0	320	US-10-732-923-23387	Sequence 23387, A
2	42	70.0	688	US-10-425-115-198285	Sequence 198285, A
3	40	66.7	89	US-09-824-438-29	Sequence 29, Appl
4	40	66.7	207	US-10-437-963-144257	Sequence 144257, A
5	40	66.7	424	US-10-369-493-7225	Sequence 7225, Ap
6	40	66.7	449	US-10-369-493-19451	Sequence 19451, A
7	40	66.7	451	US-10-369-493-4465	Sequence 4465, Ap
8	40	66.7	488	US-10-369-493-8126	Sequence 8126, Ap
9	40	66.7	519	US-10-425-115-306500	Sequence 306500, A
10	40	66.7	556	US-10-282-122A-49267	Sequence 49267, A
11	38	63.3	345	US-10-732-923-3030	Sequence 3030, Ap
12	38	63.3	457	US-10-437-963-104080	Sequence 104080, Ap
13	38	63.3	560	US-10-282-122A-55169	Sequence 55169, A
14	38	63.3	662	US-10-289-762-169	Sequence 169, App
15	38	63.3	662	US-10-282-122A-54853	Sequence 54853, A
16	37	61.7	28	US-10-362-024A-24	Sequence 24, Appl
17	37	61.7	136	US-10-425-115-283784	Sequence 283784, A
18	37	61.7	229	US-11-097-143-33174	Sequence 33174, A
19	37	61.7	296	US-10-108-260A-3020	Sequence 3020, Ap
20	37	61.7	382	US-10-739-930-7183	Sequence 7183, Ap
21	37	61.7	413	US-10-276-774-2206	Sequence 2206, Ap
22	37	61.7	452	US-10-156-761-9340	Sequence 9340, Ap
23	37	61.7	457	US-10-156-761-10667	Sequence 10667, A
24	37	61.7	482	US-10-156-761-12787	Sequence 12787, A
25	37	61.7	779	US-10-282-122A-45594	Sequence 45594, A
26	37	61.7	786	US-10-282-122A-45859	Sequence 45859, A
27	37	61.7	1836	US-09-875-363-5	Sequence 5, Appli

28	37	61.7	1836	4	US-10-162-012-24	Sequence 24, Appl
29	37	61.7	1836	4	US-10-162-102-24	Sequence 24, Appl
30	37	61.7	1836	5	US-10-723-860-329	Sequence 229, App
31	36	60.0	6	6	US-11-066-697-34	Sequence 34, Appl
32	36	60.0	7	3	US-09-953-349-6	Sequence 6, Appli
33	36	60.0	7	3	US-09-458-579-6	Sequence 6, Appli
34	36	60.0	7	4	US-10-764-712-6	Sequence 6, Appli
35	36	60.0	7	5	US-10-752-960-6	Sequence 6, Appli
36	36	60.0	17	4	US-10-181-090A-1	Sequence 1, Appli
37	36	60.0	47	4	US-10-424-599-172498	Sequence 172498, A
38	36	60.0	78	4	US-10-424-599-267678	Sequence 267678, A
39	36	60.0	94	4	US-10-425-115-276236	Sequence 276236, A
40	36	60.0	104	4	US-10-767-701-32628	Sequence 32628, A
41	36	60.0	105	3	US-09-187-693-46	Sequence 46, Appl
42	36	60.0	105	6	US-11-021-795-46	Sequence 46, Appl
43	36	60.0	114	4	US-10-424-599-245991	Sequence 245991, A
44	36	60.0	162	3	US-09-323-998D-8	Sequence 8, Appli
45	36	60.0	256	4	US-10-423-115-234798	Sequence 234798, A

ALIGNMENTS

RESULT 1
US-10-732-923-23387
; Sequence 23387, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgarton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 23387
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Lycopersicon esculentum
US-10-732-923-23387

Query Match 75.0%; Score 45; DB 5; Length 320;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YDHRWAF 8
Db 257 YDHRWFPY 264
||||| :
| :
| :
| :
| :

RESULT 2
US-10-425-115-198285
; Sequence 198285, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 198285
; LENGTH: 688
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(688)

```
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_112414C.1.pep
US-10-425-115-198285

Query Match      70.0%; Score 42; DB 4; Length 688;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YDHFRA 7
    |||||
Db 314 YDFEWA 320

RESULT 3
US-09-824-438-29
; Sequence 29, Application US/09824438
; Publication No. US20030073621A1
; GENERAL INFORMATION:
; APPLICANT: Butler, John P.
; APPLICANT: Hale, John E.
; APPLICANT: Heath Jr., William F.
; APPLICANT: Schoner, Brigitte E.
; APPLICANT: Heiman, Mark L.
; APPLICANT: Becker, Gerald W.
; APPLICANT: Varshavsky, Alexander D.
; TITLE OF INVENTION: Beta-lipotropin and Uses Thereof
; FILE REFERENCE: X-12139
; CURRENT APPLICATION NUMBER: US/09/824,438
; CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 29
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human analog
US-09-824-438-29

Query Match      66.7%; Score 40; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DHFRWA 7
    |||||
Db 46 DHFRWA 51

RESULT 4
US-10-437-963-144257
; Sequence 144257, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kowalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 144257
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:

; NAME/KEY: unsure
; LOCATION: (1)..(207)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_45089C.1.pep
US-10-437-963-144257

Query Match      66.7%; Score 40; DB 4; Length 207;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YDHFRAFX 10
    |||||
Db 89 YDVRMGFV 98

RESULT 5
US-10-369-493-7225
; Sequence 7225, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 7225
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Burkholderia cepacia
; OTHER INFORMATION: Description of Artificial Sequence: Human analog
US-10-369-493-7225

Query Match      66.7%; Score 40; DB 4; Length 424;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 DHFRWAFX 10
    |||||
Db 395 DNFWAFX 403

RESULT 6
US-10-369-493-19451
; Sequence 19451, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 19451
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
; OTHER INFORMATION: Description of Artificial Sequence: Human analog
US-10-369-493-19451
```


GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2006, 20:17:02 ; Search time 8 Seconds
(without alignments)
16.403 Million cell updates/sec

Title: HFRW
Perfect score: 60
Sequence: 1 ydhrwfafxy 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
4: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
5: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	60.0	349	7	US-11-098-686-10281
2	36	60.0	477	6	US-10-131-826A-452
3	35	58.3	396	6	US-10-467-657-280
4	35	58.3	396	6	US-10-467-657-4380
5	35	58.3	1111	7	US-11-142-700-26
6	34	56.7	15	6	US-10-939-890-198
7	34	56.7	336	7	US-11-224-260-3
8	33	55.0	188	7	US-11-234-786-592
9	33	55.0	375	6	US-10-517-939-2
10	33	55.0	422	7	US-11-230-251-26
11	33	55.0	777	7	US-11-043-693-3
12	33	55.0	1298	7	US-11-076-427A-12
13	33	55.0	1362	7	US-11-043-693-33
14	33	55.0	1363	7	US-11-043-693-32
15	33	55.0	1363	7	US-11-076-427A-10
16	33	55.0	1368	7	US-11-043-693-34
17	33	55.0	1981	6	US-10-374-954-23
18	33	55.0	1998	6	US-10-374-954-21
19	33	55.0	2009	6	US-10-374-954-2
20	32	53.3	5	7	US-11-019-955-6
21	32	53.3	13	7	US-11-019-955-4
22	32	53.3	13	7	US-11-188-552-1
23	32	53.3	13	7	US-11-188-552-71
24	32	53.3	14	7	US-11-188-552-2
25	32	53.3	14	7	US-11-188-552-3

26	32	53.3	14	7	US-11-188-552-4	Sequence 4, Appli
27	32	53.3	14	7	US-11-188-552-5	Sequence 5, Appli
28	32	53.3	14	7	US-11-188-552-6	Sequence 6, Appli
29	32	53.3	14	7	US-11-188-552-11	Sequence 11, Appl
30	32	53.3	14	7	US-11-188-552-12	Sequence 12, Appl
31	32	53.3	14	7	US-11-188-552-13	Sequence 13, Appl
32	32	53.3	17	7	US-11-083-418-4	Sequence 4, Appli
33	32	53.3	17	7	US-11-019-955-8	Sequence 8, Appli
34	32	53.3	169	7	US-11-129-143-183	Sequence 183, App
35	32	53.3	241	7	US-11-019-955-27	Sequence 27, Appl
36	32	53.3	241	7	US-11-019-955-29	Sequence 29, Appl
37	32	53.3	263	7	US-11-112-882-35	Sequence 35, Appl
38	32	53.3	263	7	US-11-166-993-120	Sequence 120, App
39	32	53.3	268	7	US-11-019-955-28	Sequence 28, Appl
40	32	53.3	315	6	US-10-524-647-25	Sequence 25, Appl
41	32	53.3	320	6	US-10-524-647-4	Sequence 4, Appli
42	32	53.3	329	6	US-10-524-647-2	Sequence 2, Appli
43	32	53.3	329	6	US-10-524-647-23	Sequence 23, Appl
44	32	53.3	329	6	US-10-524-647-80	Sequence 80, Appl
45	32	53.3	341	6	US-10-524-647-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-11-098-686-10281
; Sequence 10281, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098.686
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10281
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10281

Query Match 60.0%; Score 36; DB 7; Length 349;
Best Local Similarity 62.5%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YDHRWFAP 8
Db 40 YTHFNWKP 47

RESULT 2
US-10-131-826A-452
; Sequence 452, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven

```

; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C128
; CURRENT APPLICATION NUMBER: US/10/131.826A
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 452
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-452

```

```

Query Match 60.0%; Score 36; DB 6; Length 477;
Best Local Similarity 50.0%; Pred. No. 28;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 1 YDHRWAPFY 10
Db 35 PDGFRWDYLY 44

```

```

RESULT 3
; Sequence 280, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 280
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-280

Query Match 58.3%; Score 35; DB 6; Length 396;

```

```

Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YDHRWAF 8
Db 111 YDRFRFAF 118

```

```

RESULT 4
US-10-467-657-4380
; Sequence 4380, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4380
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4380

```

```

Query Match 58.3%; Score 35; DB 6; Length 396;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 YDHRWAF 8
Db 111 YDRFRFAF 118

```

```

RESULT 5
US-11-142-700-26
; Sequence 26, Application US/11142700
; Publication No. US20060026721A1
; GENERAL INFORMATION:
; APPLICANT: Stephen M. Allen
; APPLICANT: Gary M. Fader
; APPLICANT: Saverio Carl Falco
; APPLICANT: Anthony J. Kinney
; APPLICANT: Jonathan E. Lightner
; APPLICANT: Guo-Hua Miao
; APPLICANT: J. Antoni Rafaleski
; APPLICANT: Catherine J. Thorpe
; TITLE OF INVENTION: Plant Cellulose Synthases
; FILE REFERENCE: BB-1170
; CURRENT APPLICATION NUMBER: US/11/142,700
; CURRENT FILING DATE: 2005-06-01
; PRIOR APPLICATION NUMBER: US/09/720,383
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/092,844
; PRIOR FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 26
; LENGTH: 1111
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-142-700-26

```

```

Query Match 58.3%; Score 35; DB 7; Length 1111;
Best Local Similarity 62.5%; Pred. No. 85;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2006, 20:08:07 ; Search time 19 Seconds
(without alignments)
50.640 Million cell updates/sec

Title: HFRW

Perfect score: 60

Sequence: -1 ydfrwafxy 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	66.7	460	JC5137	beta-glucosidase (
2	39	65.0	186	T29117	hypothetical prote
3	39	65.0	320	T16358	hypothetical prote
4	39	65.0	537	T41666	carl homolog - fis
5	38	63.3	345	T07777	probable homeobox
6	38	63.3	660	A81704	DNA ligase TC0423
7	38	63.3	662	B72114	DNA ligase CP0624
8	38	63.3	662	E86509	DNA ligase (import
9	38	63.3	663	C71551	probable DNA ligas
10	37	61.7	164	G84716	hypothetical prote
11	37	61.7	311	T29111	probable beta-giuc
12	37	61.7	448	S17215	beta-glucosidase (
13	37	61.7	473	A48949	beta-glucosidase,
14	37	61.7	660	A84232	spore cortex synth
15	37	61.7	786	H69980	single-strand DNA-
16	37	61.7	1835	I34323	sodium channel alp
17	37	61.7	1836	I64893	sodium channel alp
18	37	61.7	1836	J50648	sodium channel alp
19	37	61.7	1836	I51964	sodium channel alp
20	37	61.7	1840	CHRTM1	sodium channel pro
21	37	61.7	1920	S43721	lactase (EC 3.2.1.
22	36	60.0	57	T27749	hypothetical prote
23	36	60.0	117	H71108	hypothetical prote
24	36	60.0	131	A84724	hypothetical prote
25	36	60.0	165	S37679	hypothetical prote
26	36	60.0	225	S28679	glycoprotein 30 -
27	36	60.0	324	E85513	probable integrase
28	36	60.0	324	G90662	probable integrase
29	36	60.0	408	T38386	hypothetical wd-40

30	36	60.0	434	2	S51644	secreted/adhesive
31	36	60.0	466	2	S44878	ZC262.6 protein -
32	36	60.0	477	1	A59390	probable phosphodi
33	36	60.0	477	1	A59391	probable phosphodi
34	36	60.0	477	2	JC8005	nucleotide pyropho
35	36	60.0	525	2	T32481	hypothetical prote
36	36	60.0	567	2	S69779	adhesin AP65-2 pre
37	36	60.0	567	2	S69778	adhesin AP65-1 pre
38	36	60.0	1181	2	D86157	hypothetical prote
39	36	60.0	1204	2	S62506	alpha-glucan synth
40	36	60.0	1820	1	CHEE	sodium channel pro
41	36	60.0	2049	2	T43161	sodium channel pro
42	35.5	59.2	190	2	F82810	conserved hypothet
43	35	58.3	74	2	E44103	neurocalcin gamma
44	35	58.3	148	2	F71207	hypothetical prote
45	35	58.3	166	2	AD3624	hypothetical prote

ALIGNMENTS

RESULT 1

JC5137
beta-glucosidase (EC 3.2.1.21) - Bifidobacterium breve
N:Alternate names: beta-D-glucosidase
N:Contains: beta-D-fucosidase (EC 3.2.1.38); beta-galactosidase (EC 3.2.1.23)
C:Species: Bifidobacterium breve
C:Date: 31-Jan-1997 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C:Accession: JC5137; PC4240
R:Nunoura, N.; Ohdan, K.; Tanaka, K.; Tanaki, H.; Yano, T.; Inui, M.; Yukawa, H.; Yamano Biosci. Biotechnol. Biochem. 60, 2011-2018, 1996
A:Title: Cloning and nucleotide sequence of the beta-D-glucosidase gene from Bifidobacte
A:Reference number: JC5137; MUID:97142514; PMID:8988633
A:Accession: JC5137
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-460 <NNUN1>
A:Cross-references: UNIPROT:P94248; UNIPARC:UPI000000B26ED; DDBJ:D88311; DDBJ:D84489; NID
A:Accession: PC4240
A>Status: preliminary
A:Molecule type: protein
A:Residues: 2-29 <NNUN2>
A:Cross-references: UNIPARC:UPI0000175B1B
C:Comment: This enzyme also has beta-D-fucosidase and beta-D-galactosidase activities.
C:Superfamily: Agrobacterium beta-glucosidase
C:Keywords: glycosidase; hydrolase
F:2-460/Product: beta-glucosidase #status predicted <MAT>
F:119,168/Active site: His, Glu #status predicted

Query Match 66.7%; Score 40; DB 2; Length 460;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 DHFRWAFXY 10
|:| ||| |
Db 417 DNFEWAFGY 425

RESULT 2

T29117
hypothetical protein SC1F2.08c - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T29117
R:Parkhill, J.; Barrall, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1998
A:Reference number: Z17215
A:Accession: T29117
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-186 <PAR>
A:Cross-references: UNIPROT:O86545; UNIPARC:UPI000000DAD8D; EMBL:AL031350; NID:el316892;
C:Genetics:

A;Note: SCIF2.08c

Query Match 65.0%; Score 39; DB 2; Length 186;
Best Local Similarity 75.0%; Pred. No. 9;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YDHRWAF 8
| | | | |
Db 179 YSHTRWAF 186

RESULT 3
T16358
hypothetical protein f43c9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16358
R;Fulton, B.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F43C9.
A;Reference number: Z18499
A;Accession: T16358
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-320 <FUL>
A;Cross-references: UNIPROT:Q20359; UNIPARC:UPI00000761D4; EMBL:U40427; NID:gl065557; PI
C;Genetics:
A;Gene: CESP:f43c9.1
A;Introns: 32/3; 75/3; 126/2; 155/3; 231/3; 289/3
C;Superfamily: Caenorhabditis elegans hypothetical protein f43c9.1

Query Match 65.0%; Score 39; DB 2; Length 320;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YDHRW 6
| | | | |
Db 178 FDHRW 183

RESULT 4
T41666
Carl homolog - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T41666
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
submitted to the EMBL Data Library, May 1998
A;Reference number: Z22008
A;Accession: T41666
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-537 <WOO>
A;Cross-references: UNIPROT:O59833; UNIPARC:UPI000006BBEA; EMBL:AL023590; PIDN:CAA15073-
A;Experimental source: strain 972h-; cosmid c965
C;Genetics:
A;Gene: SPDB:SPCC965.13
A;Map position: 3
C;Superfamily: benomyl/methotrexate resistance protein

Query Match 65.0%; Score 39; DB 2; Length 537;
Best Local Similarity 62.5%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YDHRWAF 8
| | | | |
Db 238 YDHRWFF 245

RESULT 5
T07777
probable homeobox protein H1 - potato
N;Alternate names: POTH1

C;Species: Solanum tuberosum (potato)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 05-Oct-2004
C;Accession: T07777
R;Hart, J.K.; Hannapel, D.J.
submitted to the EMBL Data Library, July 1996
A;Reference number: Z16126
A;Accession: T07777
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-345 <HAR>
A;Cross-references: UNIPROT:P91588; UNIPARC:UPI00000A31E3; EMBL:U65648; NID:gl814233; PI
A;Experimental source: cv. Superior; grown under short days; developmental stage: 4-day
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;262-325/Region: homeobox

Query Match 63.3%; Score 38; DB 2; Length 345;
Best Local Similarity 71.4%; Pred. No. 26;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DHRWAF 8
| | | | |
Db 284 DHRWFPY 290

RESULT 6
A81704
DNA ligase TC0423 [imported] - Chlamydia muridarum (strain Nigg)
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Dec-2004
C;Accession: A81704
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: A81704
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-660 <TET>
A;Cross-references: UNIPROT:Q9PKP2; UNIPARC:UPI0000057903; GB:AE002309; GB:AE002160; NID
A;Experimental source: strain Nigg (MoPn)
C;Genetics:
A;Gene: TC0423
C;Superfamily: DNA ligase (NAD), Liga type

Query Match 63.3%; Score 38; DB 2; Length 660;
Best Local Similarity 62.5%; Pred. No. 51;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 HFRWAFXY 10
| : | | | |
Db 301 HYRWATAY 308

RESULT 7
B72114
DNA ligase CP0624 [imported] - Chlamydophila pneumoniae (strains CWL029 and AR39)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 31-Dec-2004
C;Accession: B72114; C81556
R;Kalan, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Accession: B72114
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-662 <ARN>
A;Cross-references: UNIPROT:Q92934; UNIPARC:UPI000012967D; GB:AE001601; GB:AE001363; NID
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2006, 20:01:55 ; Search time 126.333 Seconds
(without alignments)
55.847 Million cell updates/sec

Title: HFRW
Perfect score: 60
Sequence: 1-ydhfrwaixy 10'

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	75.0	320	Q9ZRC0	LYCES
2	40	66.7	30	Q7RNH7	PLAYO
3	40	66.7	255	Q53KQ3	oryza sativ
4	40	66.7	392	Q7NKW9	gloeobacter
5	40	66.7	423	Q9A58	thermus sp.
6	40	66.7	427	Q947Z1	oryza sativ
7	40	66.7	431	Q8GEB0	thermus sp.
8	40	66.7	431	Q8GEB2	thermus fil
9	40	66.7	431	Q8GEB3	thermus the
10	40	66.7	431	Q8GEB4	thermus the
11	40	66.7	431	Q8GEB5	thermus cal
12	40	66.7	431	Q9A61	thermus the
13	40	66.7	431	Q53W75	thermus the
14	40	66.7	431	Q746L1	thermus the
15	40	66.7	436	Q9L794	thermus non
16	40	66.7	436	Q8GEB1	thermus sp.
17	40	66.7	460	P94248	bifidobacte
18	40	66.7	513	Q9ZT64	pinus conto
19	40	66.7	557	Q61029	caenorhabdi
20	40	66.7	748	Q61M36	caenorhabdi
21	39	65.0	186	Q86545	streptomyce
22	39	65.0	320	Q20359	caenorhabdi
23	39	65.0	321	Q61805	caenorhabdi
24	39	65.0	329	Q7SHA8	neurospora
25	39	65.0	334	Q6N3F8	rhodopsin
26	39	65.0	537	Q59833	schizosacch
27	39	65.0	688	Q4HKC7	campylobact
28	39	65.0	759	Q88P47	pseudomonas
29	38	63.3	144	Q5AEB6	candida alb
30	38	63.3	202	Q52BK0	magnaporthe
31	38	63.3	273	Q4MTY4	bacillus ce

32	38	63.3	278	2	Q978G1	THEVO
33	38	63.3	342	2	Q55HF8	CRYNE
34	38	63.3	342	2	Q5K6Z7	CRYPTOCOCCU
35	38	63.3	345	2	P93588	SOLANUM TUB
36	38	63.3	355	2	Q64V12	BACTEROIDES
37	38	63.3	357	2	Q5LBC9	BACTEROIDES
38	38	63.3	457	2	Q7G604	ORYZA SATIV
39	38	63.3	457	2	Q94LK1	ORYZA SATIV
40	38	63.3	646	2	Q55RH1	CRYNE
41	38	63.3	646	2	Q5KBP9	CRYNE
42	38	63.3	660	1	DNLJ	CHLMU
43	38	63.3	660	2	Q5L5Q2	CHLAB
44	38	63.3	662	1	DNLJ	CHLPN
45	38	63.3	662	2	Q822R2	CHLCV

ALIGNMENTS

RESULT 1
Q9ZRC0 LYCES
ID Q9ZRC0 LYCES PRELIMINARY; PRT; 320 AA.
AC Q9ZRC0;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Knotted 3 protein.
GN Name=TKN3;
OS Lycopersicon esculentum (Tomato)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
OX NCBI_TaxID=4081;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=sp+;
RA Parnis A., Lifschitz E.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; U76408; AAD00252.1; -; mRNA.
DR HSP; P41778; ILFU.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR005539; ELK.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR005540; KNOX2.
DR InterPro; IPR005541; KNOX2.
DR Pfam; PF03789; ELK; 1.
DR Pfam; PF03790; KNOX1; 1.
DR Pfam; PF03791; KNOX2; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; UNKNOWN_1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 320 AA; 36751 MW; 23C0FB3EEF5C5B5 CRC64;

Query Match 75.0%; Score 45; DB 2; Length 320;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YDHFRAWF 8
Db 257 YDHFRAWPY 264

RESULT 2
Q7RNH7 PLAYO
ID Q7RNH7 PLAYO PRELIMINARY; PRT; 30 AA.
AC Q7RNH7;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)

```

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Hypothetical protein (Fragment).
GN Name=PV01840.
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=71239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=2255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Anguillo S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser F.R., Bergman L.W., Vaidya A.B., O.R.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White M.J.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01000499; EAA21232.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 30 AA; 3824 MW; 9C263FA8BD58446A CRC64;

Query Match 66.7%; Score 40; DB 2; Length 30;
Best Local Similarity 60.0%; Pred. No. 7.4;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YDHFRAWFY 10
| | | | |
Db 17 YDFFDWGFSY 26

RESULT 3
Q53KQ3 ORYSA
ID Q53KQ3 ORYSA PRELIMINARY; PRT; 255 AA.
AC Q53KQ3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Retrotransposon protein, putative, unclassified.
GN ORFNames=LOC_Os11g15630;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Buell C., Yuan Q., Ouyang S., Liu J., Wang A., Maiti R., Lin H.,
RA Zhu W., Hamilton J., Jones K., Tallon L., Feldblyum T., Tsitrin T.,
RA Bera J., Kim M., Jin S., Fadresh D., Vuong H., Overton II L.,
RA Reardon M., Weaver B., Johri S., Lewis M., Utterback T., Van Aken S.,
RA Wortman J., Haas B., Koo H., Zismann V., Hsiao J., Iobst S.,
RA de Vazeilles A., White O., Salzberg S., Fraser C.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Buell R.;
RA Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC145810; AAX95906.1; -; Genomic DNA.
SQ SEQUENCE 255 AA; 30062 MW; A73924FB86E1B7E9 CRC64;

Query Match 66.7%; Score 40; DB 2; Length 255;
Best Local Similarity 50.0%; Pred. No. 62;

Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YDHFRAWFY 10
| | | | |
Db 177 YDNKWSFVY 186

RESULT 4
Q7NWK9 GLOVI
ID Q7NWK9 GLOVI PRELIMINARY; PRT; 392 AA.
AC Q7NWK9;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Grl1357 protein.
GN OrderedLocusNames=glr1357;
OS Gloeobacter violaceus.
OC Bacteria; Cyanobacteria; Gloeobacteria; Gloeobacterales; Gloeobacter.
OX NCBI_TaxID=33072;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=PCC 7421;
RX MEDLINE=22977040; PubMed=14621292;
RA Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T.,
RA Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
RA Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a
RT cyanobacterium that lacks thylakoids.";
RL DNA Res. 10:137-145(2003).
DR EMBL; BA000045; BAC89298.1; -; Genomic_DNA.
DR InterPro; IPR001173; Glyco_transf_2; I.
DR Pfam; PF00535; Glycos_transf_2; I.
DR Complete proteome.
KW Complete proteome.
SQ SEQUENCE 392 AA; 43145 MW; 25E1C2D038427DAC CRC64;

Query Match 66.7%; Score 40; DB 2; Length 392;
Best Local Similarity 62.5%; Pred. No. 95;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YDHFRAWF 8
| | | | |
Db 344 YEHLRWSP 351

RESULT 5
Q9RA58 9DEIN
ID Q9RA58 9DEIN PRELIMINARY; PRT; 423 AA.
AC Q9RA58;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-glucosidase.
OS Thermus sp. Z-1.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OX NCBI_TaxID=108325;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Z-1;
RA Takase M., Horikoshi K.;
RT "Purification and properties of a beta-glucosidase.";
RL Agric. Biol. Chem. 51:559-560(1989).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Z-1;
RA Takase M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB034947; BAA86923.1; -; Genomic_DNA.
DR HSSP; Q8GBB3; 1UG6.
DR SMR; Q9RA58; 4-423.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . . IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2006, 21:11:22 ; Search time 183 Seconds
(without alignments)

24.010 Million cell updates/sec

Title: US-10-602-394A-3

Perfect score: 53

Sequence: 1 YDRFFNAFY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*
- 9: Geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	98.1	10	9	ADW04628 Human AGR
2	52	98.1	17	9	ADW04636 Human AGR
3	45	84.9	32	3	AAB00091 Agouti re
4	45	84.9	32	3	AAB00085 Agouti re
5	42	79.2	10	9	ADW04626 Human ago
6	42	79.2	20	3	AAB00104 Agouti re
7	42	79.2	22	3	AAB00100 Agouti re
8	42	79.2	22	3	AAB00092 Agouti re
9	42	79.2	22	3	AAB00099 Agouti re
10	42	79.2	32	3	AAB00082 Agouti re
11	42	79.2	32	3	AAB00089 Agouti re
12	42	79.2	32	3	AAB00083 Agouti re
13	42	79.2	32	3	AAB00084 Agouti re
14	42	79.2	32	3	AAB00088 Agouti re
15	42	79.2	32	3	AAB00090 Agouti re
16	42	79.2	33	4	AAB75127 Human min
17	42	79.2	33	5	AAB74943 Human min
18	42	79.2	34	5	AAB74944 Human min
19	42	79.2	34	5	AAB74945 Human min
20	42	79.2	34	5	AAB75750 Human min
21	42	79.2	46	2	AAY49101 Human min
22	42	79.2	46	2	AAY49103 Mouse min
23	42	79.2	46	4	AAB75126 Human min
24	42	79.2	46	5	AAB74942 Human min

25	42	79.2	46	9	ADW04672 Human ago
26	42	79.2	47	8	ADP18425 Neurogene
27	42	79.2	48	3	AAB00081 Agouti re
28	42	79.2	50	2	AAY33951 Melanocor
29	42	79.2	54	2	AAW26778 Human ago
30	42	79.2	57	2	AAY21862 Human ago
31	42	79.2	57	2	AAY21864 Mouse ago
32	42	79.2	83	2	AAY21863 Mouse ago
33	42	79.2	83	2	AAY21861 Human ago
34	42	79.2	111	2	AAW28598 Chimeric
35	42	79.2	113	2	AAY21866 Amino aci
36	42	79.2	117	2	AAY21867 Amino aci
37	42	79.2	118	2	AAY21856 Amino aci
38	42	79.2	118	2	AAY21865 Amino aci
39	42	79.2	120	2	AAY21857 Amino aci
40	42	79.2	121	2	AAY21858 Amino aci
41	42	79.2	131	2	AAW26779 Mouse ago
42	42	79.2	131	2	AAW49104 Mouse ago
43	42	79.2	131	8	ADS87208 Murine Ag
44	42	79.2	132	2	AAW26777 Human ago
45	42	79.2	132	2	AAW26780 Human ago

ALIGNMENTS

RESULT 1
ADW04628

ID ADW04628 standard; peptide; 10 AA.

XX AC ADW04628;

DT 10-MAR-2005 (first entry)

XX Human AGRP/MCR agonist chimeric cyclic peptide #2.

DE protein engineering; melanocortin receptor; AGRP; agouti related protein;
KW obesity; gene therapy; anorectic; cyclic; melanocortin agonist.

XX Homo sapiens.

OS Chimeric.

OS Unidentified.

XX Key Location/Qualifiers

FT Misc-difference 2 /note= "this residue forms a lactam bridge with Dpr at

FT Misc-difference 9 position 9"

FT Misc-difference 9 /note= "2,3-Diaminopropionic acid (Dpr) residue forms a
lactam bridge with Asp at position 2"

FT US2004260063-A1.

XX 23-DEC-2004.

XX 23-JUN-2003; 2003US-00602394.

XX 23-JUN-2003; 2003US-00602394.

XX (HASK/) HASKELL-LUEVANO C.

XX Haskell-Luevano C;

XX WPI; 2005-030733/03.

XX New chimeric peptides and templates based upon melanocortin agonist
peptides and agouti related protein antagonist peptide, useful for
treating or preventing conditions modulated by melanocortin receptors,
such as obesity.

XX Example 3; SEQ ID NO 3; 15pp; English.

XX The present invention relates to a chimeric peptide that is biologically

CC active at melanocortin receptors (MCR) comprising an agouti (ASP) related
 CC protein (AGRP) template and melanocortin agonist-based bioactive
 CC determinant sequences which have been substituted for the analogous
 CC template sequences. The invention is useful for treating or preventing
 CC various diseases and conditions modulated by melanocortin receptors, such
 CC as obesity and in gene therapy. The present sequence is the human
 CC AGRP/MCR agonist chimeric cyclic peptide.
 XX
 SQ Sequence 10 AA;

Query Match 98.1%; Score 52; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YDRFFNAFY 10
 |||||
 Db 1 YDRFFNAFY 10

RESULT 2
 ADM04636
 ID ADM04636 standard; peptide; 17 AA.
 XX
 AC
 XX ADM04636;
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE Human AGRP/MCR agonist/NDP-MSH chimeric cyclic peptide.

XX
 KW protein engineering; melanocortin receptor; AGRP; agouti related protein;
 KW obesity; gene therapy; anorectic; cyclic; NDP-MSH; melanocortin agonist.
 XX
 OS Homo sapiens.
 OS Chimeric.
 OS Unidentified.

XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 4 /label= Nle
 FT /note= "Norleucine"
 FT Misc-difference 6 /note= "This residue forms a lactam bridge with Dpr at
 FT position 13"
 FT Misc-difference 13 /note= "2,3-Diaminopropionic acid (Dpr) residue forms a
 FT lactam bridge with Asp at position 6"
 FT Modified-site 17 /note= "C-terminal amide"
 FT
 XX US2004260063-A1.
 PN
 XX 23-DEC-2004.
 PD
 XX
 XX 23-JUN-2003; 2003US-00602394.
 PF
 XX
 XX 23-JUN-2003; 2003US-00602394.
 PR
 XX
 PA (HASK/) HASKELL-LUEVANO C.
 XX
 XX Haskell-Luevano C;
 PI
 XX WPI; 2005-030733/03.
 DR
 XX
 XX New chimeric peptides and templates based upon melanocortin agonist
 XX peptides and agouti related protein antagonist peptide, useful for
 XX treating or preventing conditions modulated by melanocortin receptors,
 XX such as obesity.
 XX
 PS Claim 7; SEQ ID NO 11; 15pp; English.
 XX
 XX The present invention relates to a chimeric peptide that is biologically

CC active at melanocortin receptors (MCR) comprising an agouti (ASP) related
 CC protein (AGRP) template and melanocortin agonist-based bioactive
 CC determinant sequences which have been substituted for the analogous
 CC template sequences. The invention is useful for treating or preventing
 CC various diseases and conditions modulated by melanocortin receptors, such
 CC as obesity and in gene therapy. The present sequence is the human
 CC AGRP/MCR agonist/NDP-MSH chimeric cyclic peptide.
 XX
 SQ Sequence 17 AA;

Query Match 98.1%; Score 52; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.03;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YDRFFNAFY 10
 |||||
 Db 5 YDRFFNAFY 14

RESULT 3
 AAB00091
 ID AAB00091 standard; peptide; 32 AA.
 XX
 AC
 XX AAB00091;
 XX
 DT 08-NOV-2000 (first entry)
 XX
 DE Agouti related peptide.

XX
 KW Agouti signalling protein; agouti related peptide; AGRP; ASP; obesity;
 KW eating disorder; antibody; probe; melanocortin; receptor.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 2 /label= Abu
 FT Modified-site 8 /label= Abu
 FT Modified-site 10 /label= Abu
 FT Modified-site 17 /label= Abu
 FT
 XX WO200044898-A2.
 PN
 XX
 XX 03-AUG-2000.
 PD
 XX
 XX 27-JAN-2000; 2000WO-US001879.
 PF
 XX
 XX 29-JAN-1999; 99US-00240078.
 PR
 XX (AMGE-) AMGEN INC.
 XX
 XX Jarosinski MA;
 PI
 XX WPI; 2000-476223/41.
 DR
 XX N-PSDB; AAA47812.
 DR
 XX Novel peptides derived from human anti-agouti-related polypeptide and
 XX anti-agouti-signaling protein, useful for treating eating disorders, e.g.
 XX obesity.
 XX
 PS Claim 1; Page 50; 81pp; English.
 XX
 XX Agouti related peptides, their fragments, variants or derivatives may be
 XX used as modulators of feeding behavior (e.g. to treat obesity) and to
 XX generate anti-agouti-related polypeptide (AGRP) and anti-agouti-signaling
 XX protein (ASP) antibodies. Nucleic acids encoding these peptides may be
 XX used as hybridization probes in assays. The antibodies may be used to
 XX inhibit the binding of the AGRP/ASP peptide to melanocortin receptors or
 XX in vitro or in vivo diagnostics. This sequence corresponds to amino
 XX acids 81-112 of human AGRP with amino acids 82, 88, 90 and 97 of native

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2006, 21:18:47 ; Search time 47 Seconds
(without alignments)
17.591 Million cell updates/sec

Title: US-10-602-394A-3
Perfect score: 53
Sequence: 1 YDRFFNAFY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	84.9	32	2	US-09-240-078-5
2	45	84.9	32	2	US-09-240-078-11
3	42	79.2	20	2	US-09-240-078-24
4	42	79.2	22	2	US-09-240-078-12
5	42	79.2	22	2	US-09-240-078-19
6	42	79.2	22	2	US-09-240-078-20
7	42	79.2	32	2	US-09-240-078-2
8	42	79.2	32	2	US-09-240-078-3
9	42	79.2	32	2	US-09-240-078-4
10	42	79.2	32	2	US-09-240-078-8
11	42	79.2	32	2	US-09-240-078-9
12	42	79.2	32	2	US-09-240-078-10
13	42	79.2	48	2	US-09-240-078-1
14	42	79.2	50	2	US-09-031-902-2
15	42	79.2	54	1	US-08-757-541-8
16	42	79.2	54	2	US-09-033-275-8
17	42	79.2	54	2	US-09-342-581-8
18	42	79.2	57	2	US-09-581-894A-7
19	42	79.2	57	2	US-09-581-894A-9
20	42	79.2	83	2	US-09-581-894A-6
21	42	79.2	83	2	US-09-581-894A-8
22	42	79.2	113	2	US-09-581-894A-11
23	42	79.2	117	2	US-09-581-894A-12
24	42	79.2	118	2	US-09-581-894A-1
25	42	79.2	118	2	US-09-581-894A-10
26	42	79.2	120	2	US-09-581-894A-2
27	42	79.2	121	2	US-09-581-894A-3

28	42	79.2	131	1	US-08-757-541-10	Sequence 10, Appl
29	42	79.2	131	2	US-09-033-275-10	Sequence 10, Appl
30	42	79.2	131	2	US-09-342-581-10	Sequence 10, Appl
31	42	79.2	132	1	US-08-757-541-7	Sequence 7, Appl
32	42	79.2	132	1	US-08-757-541-11	Sequence 11, Appl
33	42	79.2	132	2	US-09-033-275-7	Sequence 7, Appl
34	42	79.2	132	2	US-09-033-275-11	Sequence 11, Appl
35	42	79.2	132	2	US-09-342-581-7	Sequence 7, Appl
36	42	79.2	132	2	US-09-342-581-11	Sequence 11, Appl
37	42	79.2	132	2	US-09-342-581-10	Sequence 10, Appl
38	42	79.2	605	2	US-09-581-894A-15	Sequence 15, Appl
39	42	79.2	620	2	US-09-581-894A-13	Sequence 13, Appl
40	42	79.2	621	2	US-09-581-894A-17	Sequence 17, Appl
41	42	79.2	621	2	US-09-581-894A-19	Sequence 19, Appl
42	42	79.2	654	2	US-09-581-894A-4	Sequence 4, Appl
43	42	79.2	666	2	US-09-581-894A-16	Sequence 16, Appl
44	42	79.2	683	2	US-09-581-894A-14	Sequence 14, Appl
45	42	79.2	684	2	US-09-581-894A-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-09-240-078-5
; Sequence 5, Application US/09240078
; Patent No. 6303749
; GENERAL INFORMATION:
; APPLICANT: Jarosinski, Mark A.
; TITLE OF INVENTION: No. 6303749el Agouti and Agouti-Related Peptide Analogs
; FILE REFERENCE: A-569
; CURRENT APPLICATION NUMBER: US/09/240,078
; CURRENT FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AGRP Peptide
; OTHER INFORMATION: Analog with synthetic amino acid (amino butyric
; OTHER INFORMATION: acid) at positions 12, 15, 20 and 27 and labeled
; OTHER INFORMATION: as Xaa.
US-09-240-078-5

Query Match 84.9%; Score 45; DB 2; Length 32;
Best Local Similarity 90.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YDRFFNAFY 10
| | | | | | | | | |
Db 19 YXRFNAPFY 28

RESULT 2
US-09-240-078-11
; Sequence 11, Application US/09240078
; Patent No. 6303749
; GENERAL INFORMATION:
; APPLICANT: Jarosinski, Mark A.
; TITLE OF INVENTION: No. 6303749el Agouti and Agouti-Related Peptide Analogs
; FILE REFERENCE: A-569
; CURRENT APPLICATION NUMBER: US/09/240,078
; CURRENT FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AGRP Peptide

```
; OTHER INFORMATION: Analog with synthetic amino acid (amino butyric
; OTHER INFORMATION: acid) located at positions 2, 8, 10 and 17 and
; OTHER INFORMATION: labeled as Xaa.
US-09-240-078-11

Query Match      84.9%; Score 45; DB 2; Length 32;
Best Local Similarity 90.0%; Pred. No. 0.22; 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YDRFFNAFY 10
Db 9 YCRFFNAFY 18

RESULT 3
US-09-240-078-24
; Sequence 24, Application US/09240078
; Patent No. 6303749
; GENERAL INFORMATION:
; APPLICANT: Jarosinski, Mark A.
; TITLE OF INVENTION: No. 6303749el Agouti and Agouti-Related Peptide Analogs
; FILE REFERENCE: A-569
; CURRENT APPLICATION NUMBER: US/09/240,078
; CURRENT FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AGRP Peptide
; OTHER INFORMATION: Analog with amino acids located at positions 3, 6,
; OTHER INFORMATION: and 17 replaced by alanine (Ala) and in which the
; OTHER INFORMATION: amino terminus is acetylated..
US-09-240-078-24

Query Match      79.2%; Score 42; DB 2; Length 20;
Best Local Similarity 80.0%; Pred. No. 0.47; 2; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YDRFFNAFY 10
Db 7 YCRFFNAFY 16

RESULT 4
US-09-240-078-12
; Sequence 12, Application US/09240078
; Patent No. 6303749
; GENERAL INFORMATION:
; APPLICANT: Jarosinski, Mark A.
; TITLE OF INVENTION: No. 6303749el Agouti and Agouti-Related Peptide Analogs
; FILE REFERENCE: A-569
; CURRENT APPLICATION NUMBER: US/09/240,078
; CURRENT FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AGRP Peptide
; OTHER INFORMATION: Analog with synthetic amino acid (amino butyric
; OTHER INFORMATION: acid) located at positions 2, 5, and 8 and labeled
; OTHER INFORMATION: as Xaa.
US-09-240-078-12

Query Match      79.2%; Score 42; DB 2; Length 22;
Best Local Similarity 80.0%; Pred. No. 0.52; 2; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YDRFFNAFY 10
Db 9 YCRFFNAFY 18

RESULT 5
US-09-240-078-19
; Sequence 19, Application US/09240078
; Patent No. 6303749
; GENERAL INFORMATION:
; APPLICANT: Jarosinski, Mark A.
; TITLE OF INVENTION: No. 6303749el Agouti and Agouti-Related Peptide Analogs
; FILE REFERENCE: A-569
; CURRENT APPLICATION NUMBER: US/09/240,078
; CURRENT FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AGRP Peptide
; OTHER INFORMATION: Analog with amino acids located at positions 2, 5
; OTHER INFORMATION: and 8 replaced by alanine (Ala).
US-09-240-078-19

Query Match      79.2%; Score 42; DB 2; Length 22;
Best Local Similarity 80.0%; Pred. No. 0.52; 2; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YDRFFNAFY 10
Db 9 YCRFFNAFY 18

RESULT 6
US-09-240-078-20
; Sequence 20, Application US/09240078
; Patent No. 6303749
; GENERAL INFORMATION:
; APPLICANT: Jarosinski, Mark A.
; TITLE OF INVENTION: No. 6303749el Agouti and Agouti-Related Peptide Analogs
; FILE REFERENCE: A-569
; CURRENT APPLICATION NUMBER: US/09/240,078
; CURRENT FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AGRP Peptide
; OTHER INFORMATION: Analog with amino acids located at positions 2, 3,
; OTHER INFORMATION: 5 and 8 replaced by alanine (Ala).
US-09-240-078-20

Query Match      79.2%; Score 42; DB 2; Length 22;
Best Local Similarity 80.0%; Pred. No. 0.52; 2; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YDRFFNAFY 10
Db 9 YCRFFNAFY 18

RESULT 7
US-09-240-078-2
; Sequence 2, Application US/09240078
; Patent No. 6303749
; GENERAL INFORMATION:
; APPLICANT: Jarosinski, Mark A.
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2006, 21:29:57 ; Search time 164 Seconds
(without alignments)
25.477 Million cell updates/sec

Title: US-10-602-394A-3
Perfect score: 53
Sequence: 1 YDRFFNAFYX 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569.

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	79.2	33	US-09-851-586A-3	Sequence 3, Appli
2	42	79.2	34	US-09-851-586A-4	Sequence 4, Appli
3	42	79.2	34	US-09-851-586A-5	Sequence 5, Appli
4	42	79.2	46	US-09-851-586A-2	Sequence 2, Appli
5	42	79.2	47	US-10-718-071-39	Sequence 39, Appli
6	42	79.2	54	US-09-754-862-8	Sequence 8, Appli
7	42	79.2	54	US-10-256-590-8	Sequence 8, Appli
8	42	79.2	131	US-09-754-862-10	Sequence 10, Appli
9	42	79.2	131	US-10-256-590-10	Sequence 10, Appli
10	42	79.2	132	US-09-754-862-7	Sequence 7, Appli
11	42	79.2	132	US-09-754-862-11	Sequence 11, Appli
12	42	79.2	132	US-09-851-586A-1	Sequence 1, Appli
13	42	79.2	132	US-10-207-330-10	Sequence 10, Appli
14	42	79.2	132	US-10-256-590-7	Sequence 7, Appli
15	42	79.2	132	US-10-256-590-11	Sequence 11, Appli
16	42	79.2	132	US-10-379-747-26	Sequence 26, Appli
17	42	79.2	132	US-11-060-291-10	Sequence 10, Appli
18	40	75.5	484	US-10-425-114-49505	Sequence 49505, A
19	40	75.5	728	US-10-424-599-189465	Sequence 189465,
20	39	73.6	339	US-10-739-930-5959	Sequence 5959, Ap
21	37	69.8	604	US-10-424-599-207219	Sequence 207219,
22	37	69.8	1548	US-10-437-963-112738	Sequence 112738,
23	36	67.9	38	US-10-424-599-200686	Sequence 200686,
24	36	67.9	360	US-10-282-122A-68814	Sequence 68814, A
25	36	67.9	460	US-10-369-493-5817	Sequence 5817, Ap
26	36	67.9	733	US-10-437-963-171240	Sequence 171240,
27	36	67.9	812	US-10-437-963-123561	Sequence 123561,

28	36	67.9	885	4	US-10-437-963-171263	Sequence 171263,
29	35	66.0	117	3	US-09-881-752A-232	Sequence 232, App
30	35	66.0	516	3	US-09-430-029-5	Sequence 5, Appli
31	35	66.0	800	6	US-11-097-143-15480	Sequence 15480, A
32	35	66.0	1239	4	US-10-425-115-303754	Sequence 303754,
33	35	66.0	1683	4	US-10-369-493-22273	Sequence 22273, A
34	34	64.2	12	5	US-10-771-232-19	Sequence 19, Appl
35	34	64.2	62	4	US-10-424-599-245398	Sequence 245398,
36	34	64.2	71	4	US-10-437-963-200519	Sequence 200519,
37	34	64.2	82	4	US-10-425-115-34841	Sequence 34841,
38	34	64.2	101	4	US-10-282-122A-57526	Sequence 57526, A
39	34	64.2	138	4	US-10-767-701-43254	Sequence 43254, A
40	34	64.2	155	4	US-10-424-599-278805	Sequence 278805,
41	34	64.2	201	4	US-10-282-122A-67733	Sequence 67733, A
42	34	64.2	202	4	US-10-282-122A-48979	Sequence 48979, A
43	34	64.2	207	4	US-10-282-122A-69731	Sequence 69731, A
44	34	64.2	208	4	US-10-282-122A-47739	Sequence 47739, A
45	34	64.2	208	4	US-10-282-122A-54542	Sequence 54542, A

ALIGNMENTS

RESULT 1
US-09-851-586A-3
; Sequence 3, Application US/09851586A
; Publication No. US20030064921A1
; GENERAL INFORMATION:
; APPLICANT: MILLHAUSER, GLENN
; APPLICANT: THOMPSON, DARREN
; APPLICANT: BOLIN, KIMBERLEY
; APPLICANT: ANDERSON, JOE
; APPLICANT: MCNUITY, JOSEPH
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING MELANOCORTIN RECEPTOR LIGAN

; FILE REFERENCE: 407t-980910US
; CURRENT APPLICATION NUMBER: US/09/851,586A
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: PCT/US99/25201
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/203,271
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 60/226,047
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-851-586A-3

Query Match 79.2%; Score 42; DB 3; Length 33;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YDRFFNAFYX 10
Db 23 YCRFFNAFCY 32

RESULT 2
US-09-851-586A-4
; Sequence 4, Application US/09851586A
; Publication No. US20030064921A1
; GENERAL INFORMATION:
; APPLICANT: MILLHAUSER, GLENN
; APPLICANT: THOMPSON, DARREN
; APPLICANT: BOLIN, KIMBERLEY
; APPLICANT: ANDERSON, JOE
; APPLICANT: MCNUITY, JOSEPH
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING MELANOCORTIN RECEPTOR LIGAN

FILE REFERENCE: 407t-980910US
CURRENT APPLICATION NUMBER: US/09/851,586A
CURRENT FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: PCT/US99/25201
PRIOR FILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: 60/203,271
PRIOR FILING DATE: 2000-05-09
PRIOR APPLICATION NUMBER: 60/226,047
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 34
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic mini-AGRP
US-09-851-586A-4

Query Match 79.2%; Score 42; DB 3; Length 34;
Best Local Similarity 80.0%; Pred. No. 1.5; Length 34;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YDRFFNAFY 10
| | | | | | | |
Db 23 YCRFFNAFCY 32

RESULT 3

US-09-851-586A-5
Sequence 5, Application US/09851586A
Publication No. US20030064921A1
GENERAL INFORMATION:
APPLICANT: MILLHAUSER, GLENN
APPLICANT: THOMPSON, DARREN
APPLICANT: BOLIN, KIMBERLEY
APPLICANT: ANDERSON, JOE
APPLICANT: MCNUITY, JOSEPH
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING MELANOCORTIN RECEPTOR LIGAND
TITLE OF INVENTION: AND ACTIVITY
FILE REFERENCE: 407t-980910US
CURRENT APPLICATION NUMBER: US/09/851,586A
CURRENT FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: PCT/US99/25201
PRIOR FILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: 60/203,271
PRIOR FILING DATE: 2000-05-09
PRIOR APPLICATION NUMBER: 60/226,047
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 34
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic AGRP fragment
FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: C blocked with acetyl
FEATURE:
NAME/KEY: MOD RES
LOCATION: (34)..(34)
OTHER INFORMATION: R blocked with amino
US-09-851-586A-5

Query Match 79.2%; Score 42; DB 3; Length 34;
Best Local Similarity 80.0%; Pred. No. 1.5; Length 34;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YDRFFNAFY 10
| | | | | | | |

Db 23 YCRFFNAFCY 32

RESULT 4

US-09-851-586A-2
Sequence 2, Application US/09851586A
Publication No. US20030064921A1
GENERAL INFORMATION:
APPLICANT: MILLHAUSER, GLENN
APPLICANT: THOMPSON, DARREN
APPLICANT: BOLIN, KIMBERLEY
APPLICANT: ANDERSON, JOE
APPLICANT: MCNUITY, JOSEPH
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING MELANOCORTIN RECEPTOR LIGAND
TITLE OF INVENTION: AND ACTIVITY
FILE REFERENCE: 407t-980910US
CURRENT APPLICATION NUMBER: US/09/851,586A
CURRENT FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: PCT/US99/25201
PRIOR FILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: 60/203,271
PRIOR FILING DATE: 2000-05-09
PRIOR APPLICATION NUMBER: 60/226,047
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 46
TYPE: PRT
ORGANISM: Homo sapiens
US-09-851-586A-2

Query Match 79.2%; Score 42; DB 3; Length 46;
Best Local Similarity 80.0%; Pred. No. 2; Length 46;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YDRFFNAFY 10
| | | | | | | |
Db 23 YCRFFNAFCY 32

RESULT 5

US-10-718-071-39
Sequence 39, Application US/10718071
Publication No. US20050009847A1
GENERAL INFORMATION:
APPLICANT: Bertilsson, Goran
APPLICANT: Erlandsson, Rikard
APPLICANT: Frisen, Jonas
APPLICANT: Haegerstrand, Anders
APPLICANT: Heidrich, Jessica
APPLICANT: Hellstrom, Kristina
APPLICANT: Haggblad, Johan
APPLICANT: Jansson, Katarina
APPLICANT: Kortesmaa, Jarkko
APPLICANT: Lindquist, Per
APPLICANT: Lundh, Hanna
APPLICANT: McGuire, Jacqueline
APPLICANT: Mercer, Alex
APPLICANT: Nyberg, Karl
APPLICANT: Ossoinak, Amina
APPLICANT: Patrone, Cesare
APPLICANT: Ronnhelm, Harriet
APPLICANT: Wikstrom, Lillian
APPLICANT: Zachrisson, Olof
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INCREASING NEUROGENESIS
FILE REFERENCE: 21882-517 UTIL
CURRENT APPLICATION NUMBER: US/10/718,071
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: US 60/427,912
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.2

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2006, 21:30:32 ; Search time 16 Seconds
(without alignments)
8.202 Million cell updates/sec

Title: US-10-602-394A-3

Perfect score: 53

Sequence: 1 YDRFFNAFY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	79.2	46	7	US-11-188-552-70
2	42	79.2	50	7	US-11-188-552-69
3	42	79.2	50	7	US-11-174-845-2
4	42	79.2	50	7	US-11-174-851-2
5	42	79.2	131	6	US-10-518-955-2
6	42	79.2	132	6	US-10-518-955-4
7	34	64.2	305	7	US-11-156-084-186
8	34	64.2	389	7	US-11-129-143-81
9	33	62.3	32	6	US-10-895-064-2411
10	33	62.3	109	7	US-11-156-084-139
11	33	62.3	286	7	US-11-057-012-93
12	33	62.3	350	6	US-10-467-657-3588
13	32	60.4	267	7	US-11-052-554A-300
14	31	58.5	233	6	US-10-467-657-8268
15	31	58.5	286	6	US-10-793-626-2192
16	31	58.5	691	6	US-10-467-657-7170
17	30.5	57.5	607	6	US-10-131-826A-344
18	30.5	57.5	607	7	US-11-176-863-2
19	30	56.6	350	6	US-10-467-657-224
20	30	56.6	350	6	US-10-467-657-512
21	30	56.6	375	6	US-10-517-939-2
22	30	56.6	802	6	US-10-510-386-2
23	30	56.6	1400	6	US-10-821-234-1045
24	29	54.7	134	6	US-10-793-626-3006
25	29	54.7	134	6	US-10-793-626-3046

26	29	54.7	134	6	US-10-793-626-3304	Sequence 3304, Ap
27	29	54.7	162	5	US-09-978-360A-732	Sequence 732, App
28	29	54.7	267	6	US-10-873-528-101	Sequence 101, App
29	29	54.7	321	6	US-10-467-657-2352	Sequence 2352, Ap
30	29	54.7	322	7	US-11-156-084-318	Sequence 318, App
31	29	54.7	354	6	US-10-467-657-4352	Sequence 4352, Ap
32	29	54.7	360	7	US-11-194-246-321	Sequence 321, App
33	29	54.7	424	7	US-11-055-822-1036	Sequence 1036, Ap
34	29	54.7	497	6	US-10-454-437-410	Sequence 410, App
35	29	54.7	644	6	US-10-467-657-5958	Sequence 5958, Ap
36	29	54.7	757	7	US-11-097-463-2	Sequence 2, Appli
37	29	54.7	844	7	US-11-097-463-4	Sequence 4, Appli
38	29	54.7	846	6	US-10-517-939-90	Sequence 90, Appl
39	29	54.7	1102	7	US-11-098-686-10951	Sequence 10951, A
40	28	52.8	114	5	US-09-978-360A-726	Sequence 726, App
41	28	52.8	116	6	US-10-467-657-7486	Sequence 7486, Ap
42	28	52.8	118	7	US-11-049-536-606	Sequence 606, App
43	28	52.8	138	7	US-11-098-686-11366	Sequence 11366, A
44	28	52.8	147	6	US-10-485-517-343	Sequence 343, App
45	28	52.8	155	6	US-10-467-657-1206	Sequence 1206, Ap

ALIGNMENTS

RESULT 1
US-11-188-552-70
; Sequence 70, Application US/11188552
; Publication No. US20050282739A1
; GENERAL INFORMATION:
; APPLICANT: Palatin Technologies, Inc.
; APPLICANT: Sharma, Shubh
; APPLICANT: Shi, Yi-Qun
; APPLICANT: Bastos, Margarita
; APPLICANT: Rajpurohit, Ramesh
; APPLICANT: Cai, Hui-Zhi
; TITLE OF INVENTION: Metallopeptide Compounds
; FILE REFERENCE: 0507-05
; CURRENT APPLICATION NUMBER: US/11/188,552
; CURRENT FILING DATE: 2005-07-25
; PRIOR APPLICATION NUMBER: US 60/590,933
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US 10/769,695
; PRIOR FILING DATE: 2005-01-30
; PRIOR APPLICATION NUMBER: US 60/444,129
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 10/464,117
; PRIOR FILING DATE: 2003-06-17
; PRIOR APPLICATION NUMBER: PCT/US01/50075
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 60/256,842
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 60/304,835
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 60/327,835
; PRIOR FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 70
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-188-552-70

Query Match 79.2%; Score 42; DB 7; Length 46;
Best-Local Similarity 80.0%; Pred.No. 0.15;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YDRFFNAFY 10
| | | | | | | |
Db 23 YCRFFNAFCY 32

```
RESULT 2
US-11-188-552-69
; Sequence 69, Application US/11188552
; Publication No. US20050282739A1
; GENERAL INFORMATION:
; APPLICANT: Palatin Technologies, Inc.
; APPLICANT: Sharma, Shubh
; APPLICANT: Shi, Yi-Qun
; APPLICANT: Bastos, Margarita
; APPLICANT: Rajpurohit, Ramesh
; APPLICANT: Cai, Hui-Zhi
; TITLE OF INVENTION: Metallopeptide Compounds
; FILE REFERENCE: 0507-05
; CURRENT APPLICATION NUMBER: US/11/188,552
; CURRENT FILING DATE: 2005-07-25
; PRIOR APPLICATION NUMBER: US 60/590,933
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US 10/769,695
; PRIOR FILING DATE: 2005-01-30
; PRIOR APPLICATION NUMBER: US 60/444,129
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 10/464,117
; PRIOR FILING DATE: 2003-06-17
; PRIOR APPLICATION NUMBER: PCT/US01/50075
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 60/256,842
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 60/304,835
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 60/327,835
; PRIOR FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 69
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-188-552-69

Query Match      79.2%; Score 42; DB 7; Length 50;
Best Local Similarity 80.0%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 YDRFFNAFY 10
        |||||||
DB      27 YCRFFNAFCY 36

RESULT 3
US-11-174-845-2
; Sequence 2, Application US/11174845
; Publication No. US20060014676A1
; GENERAL INFORMATION:
; APPLICANT: Palatin Technologies, Inc.
; APPLICANT: Sharma, Shubh D.
; APPLICANT: Rajpurohit, Ramesh
; APPLICANT: Shaddack, Annette M.
; APPLICANT: Shi, Yi-Qun
; APPLICANT: Burtis, Kevin B.
; TITLE OF INVENTION: Cyclic Peptides for Treatment of Cachexia
; FILE REFERENCE: 70025-US05-071
; CURRENT APPLICATION NUMBER: US/11/174,845
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,791
; PRIOR FILING DATE: 2004-07-06
; PRIOR APPLICATION NUMBER: US 10/638,071
; PRIOR FILING DATE: 2003-08-03
; PRIOR APPLICATION NUMBER: PCT/US02/22196
; PRIOR FILING DATE: 2002-07-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-174-845-2

Query Match      79.2%; Score 42; DB 7; Length 50;
Best Local Similarity 80.0%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 YDRFFNAFY 10
        |||||||
DB      27 YCRFFNAFCY 36

RESULT 4
US-11-174-851-2
; Sequence 2, Application US/11174851
; Publication No. US20060014194A1
; GENERAL INFORMATION:
; APPLICANT: Palatin Technologies, Inc.
; APPLICANT: Sharma, Shubh D.
; APPLICANT: Rajpurohit, Ramesh
; APPLICANT: Shaddack, Annette M.
; APPLICANT: Shi, Yi-Qun
; APPLICANT: Burtis, Kevin B.
; TITLE OF INVENTION: Cyclic Peptides for Treatment of Cachexia
; FILE REFERENCE: 70025-US05-0707
; CURRENT APPLICATION NUMBER: US/11/174,851
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,791
; PRIOR FILING DATE: 2004-07-06
; PRIOR APPLICATION NUMBER: US 10/638,071
; PRIOR FILING DATE: 2003-08-03
; PRIOR APPLICATION NUMBER: PCT/US02/22196
; PRIOR FILING DATE: 2002-07-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-174-851-2

Query Match      79.2%; Score 42; DB 7; Length 50;
Best Local Similarity 80.0%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 YDRFFNAFY 10
        |||||||
DB      27 YCRFFNAFCY 36

RESULT 5
US-10-518-955-2
; Sequence 2, Application US/10518955
; Publication No. US20050257279A1
; GENERAL INFORMATION:
; APPLICANT: Qian, Su
; APPLICANT: Van der Ploeg, Leonardus, H.T.
; APPLICANT: Chen, Howard
; APPLICANT: Weingarth, Drew T.
; APPLICANT: Trumbauer, Myrna
; APPLICANT: Metzger, Joseph M.
; TITLE OF INVENTION: Agouti-related protein deficient cells,
; TITLE OF INVENTION: non-human transgenic animals and methods of selecting
; TITLE OF INVENTION: compounds which regulate energy metabolism
; FILE REFERENCE: 21033YP
; CURRENT APPLICATION NUMBER: US/10/518,955
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/US03/20245
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/393,391
; PRIOR FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 14
; LENGTH: 50
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2006, 21:14:52 ; Search time 38 Seconds
(without alignments)
25.320 Million cell updates/sec

Title: US-10-602-394A-3
Perfect score: 53
Sequence: 1 YDRFFNAFY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	40	75.5	548	2	T18761	hypothetical prote
2	38	71.7	118	2	T1818	hypothetical prote
3	38	71.7	282	2	F86786	GTP-binding protei
4	37	69.8	653	2	D69815	conserved hypotet
5	36	67.9	389	2	S31123	hypothetical prote
6	36	67.9	408	2	H71672	ampg protein (ampG
7	36	67.9	460	2	F88544	protein F59B2.2 [i
8	36	67.9	3394	2	T18501	hypothetical prote
9	35	66.0	117	2	A84701	conserved hypotet
10	35	66.0	252	2	B71105	hypothetical prote
11	35	66.0	301	2	T24993	hypothetical prote
12	35	66.0	392	2	B70242	conserved hypotet
13	35	66.0	641	2	JC7142	dextranase (EC 3.2
14	35	66.0	863	2	G36964	probable permease,
15	35	66.0	1683	2	S38103	Spo14 protein - ye
16	34	64.2	160	2	S77324	hypothetical prote
17	34	64.2	208	2	B81327	hypothetical prote
18	34	64.2	234	2	AF3543	phosphoglycolate p
19	34	64.2	271	2	H70888	hypothetical prote
20	34	64.2	280	2	F70805	hypothetical prote
21	34	64.2	305	2	C72366	tRNA delta-2-isope
22	34	64.2	328	2	A13541	NADH2 dehydrogenas
23	34	64.2	478	2	H50246	hypothetical prote
24	34	64.2	499	2	S52422	chitinase (EC 3.2.
25	34	64.2	499	2	S04856	chitinase (EC 3.2.
26	34	64.2	616	2	S64156	probable membrane
27	34	64.2	653	2	AG1190	hypothetical trans
28	34	64.2	653	2	AG1548	hypothetical trans
29	34	64.2	913	2	JG0168	gob-5 protein - mo

30	64.2	1596	2	AG2501	hypothetical prote
31	64.2	4981	2	T18489	hypothetical prote
32	62.3	104	2	S59108	hypothetical prote
33	62.3	168	2	D87310	hypothetical prote
34	62.3	205	2	H86767	hypothetical prote
35	62.3	248	2	A46652	glucosamine-6-phos
36	62.3	281	2	G87451	hypothetical prote
37	62.3	283	2	C98002	conserved hypotet
38	62.3	283	2	G95133	GTP-binding protei
39	62.3	294	2	A57478	serine O-acetyltra
40	62.3	298	2	T33317	hypothetical prote
41	62.3	341	2	I57997	hypothetical calci
42	62.3	343	2	D69482	hypothetical prote
43	62.3	396	2	T33315	hypothetical prote
44	62.3	415	2	D95248	conserved hypotet
45	62.3	415	2	A98113	conserved hypotet

ALIGNMENTS

RESULT 1
T18761
Hypothetical protein B0462.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18761
R;Mortimore, B.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19018
A;Accession: T18761
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-548 <WIL>
A;Cross-references: UNIPROT:O62019; UNIPARC:UPI00000077D6B; EMBL:Z81456; PIDN:CAB03810.1
A;Experimental source: clone B0462
C;Genetics:
A;Gene: CESP:B0462.1
A;Map position: 5
A;Introns: 21/1; 93/3; 135/3; 164/3; 289/3; 372/2

Query Match 75.5%; Score 40; DB 2; Length 548;
Best Local Similarity 77.8%; Pred. No. 8.8;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DRFPNAPXY 10
:|||||
Db 539 ERFNAPCY 547

RESULT 2
D71818
Hypothetical protein jhp1342 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: D71818
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Millis, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric pat
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: D71818
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-118 <ARN>
A;Cross-references: UNIPROT:Q9ZJG9; UNIPARC:UPI000013AAE7; GB:AE001557; GB:AE001439; NI
A;Experimental source: strain J99
C;Genetics:
A;Gene: jhp1342
C;Superfamily: conserved hypothetical protein HI1000
Query Match 71.7%; Score 38; DB 2; Length 118;

Best Local Similarity 60.0%; Pred. No. 4.3;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YDRFFNAPFY 10
| | | | |
Db 20 YORFFSAFTF 29

RESULT 3
GTP-binding protein [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Dec-2004
C:Accession: F86786
R:Boilotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: F86786
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-282 <STO>
A:Cross-references: UNIPROT:Q9CG16; UNIPARC:UPI0000069FE; GB:AE005176; PID:g12724271; F
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: yJqL
C:Superfamily: GTPases

Query Match 71.7%; Score 38; DB 2; Length 282;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YDRFFNAPF 8
| | | | |
Db 253 YDRFFNMF 260

RESULT 4
D69815
conserved hypothetical protein yfni - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004
C:Accession: D69815
R:Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabbret, C.; Ferrati, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritze, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
iech, J.; Harwood, C.R.; Hensaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpsira, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yanane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: D69815
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-653 <KUN>
A:Cross-references: UNIPROT:Q06487; UNIPARC:UPI000006006F; GB:Z99107; GB:AL009126; NID:9
A:Experimental source: strain 168
C:Genetics:
A:Gene: yfni
C:Superfamily: membrane sulfatase, H1246 type

Query Match 69.8%; Score 37; DB 2; Length 653;
Best Local Similarity 60.0%; Pred. No. 38;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YDRFFNAPFY 10
| | | | |
Db 376 YDRFFDASTY 385

RESULT 5
S31123
hypothetical protein F59B2.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S31123
R:Sulston, J.; Du, Z.; Thomas, K.; Wilson, R.; Hillier, L.; Staden, R.; Halloran, N.; Gr
awkins, T.; Ainscough, R.; Waterston, R.
submitted to the EMBL Data Library, November 1991
A:Description: The C. elegans sequencing project: A beginning.
A:Reference number: S31122
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-389 <SUL>
A:Cross-references: UNIPROT:P34479; UNIPARC:UPI000017BA50; EMBL:Z11505; NID:g6718; PID:g
C:Genetics:
A:Introns: 38/2; 59/2; 148/2; 343/3

Query Match 67.9%; Score 36; DB 2; Length 389;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YDRFFNAPF 8
| | | | |
Db 265 YDMFFNGF 272

RESULT 6
H71672
ampg protein (ampG2) RP668 - Rickettsia prowazekii
C:Species: Rickettsia prowazekii
C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C:Accession: H71672
R:Andersson, S.G.B.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alemark, U
Nature 396, 133-140, 1998
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A:Reference number: A71630; MUID:99039499; PMID:9823893
A:Accession: H71672
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-408 <AND>
A:Cross-references: UNIPROT:Q9ZCQ1; UNIPARC:UPI000000D37DA; GB:AJ235272; GB:AJ235269; NID
A:Experimental source: strain Madrid E
C:Genetics:
A:Gene: ampg2; RP668

Query Match 67.9%; Score 36; DB 2; Length 408;
Best Local Similarity 75.0%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YDRFFNAPF 8
| | | | |
Db 208 DFRFLNAPF 215

RESULT 7
F88544
protein F59B2.2 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: F88544
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2006, 21:11:37 ; Search time 229 Seconds
(without alignments)
30.809 Million cell updates/sec

Title: US-10-602-394A-3
Perfect score: 53
Sequence: 1 YDRFFNAPFY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	79.2	71	2 Q90WY7 COTJA	Q90WY7 coturnix co
2	42	79.2	105	2 Q6J648 SHEEP	Q6J648 ovis aries
3	42	79.2	121	2 Q9GLM5 PIG	Q9GLM5 sus scrofa
4	42	79.2	131	1 AGRP MOUSE	P56473 mus musculus
5	42	79.2	132	1 AGRP HUMAN	O00253 homo sapien
6	42	79.2	134	1 AGRP BOVIN	P56413 bos taurus
7	42	79.2	134	1 AGRP PIG	Q9CUL8 sus scrofa
8	42	79.2	154	2 Q9PWG2 CHICK	Q9PWG2 gallus gall
9	42	79.2	165	2 Q9W7R0 CHICK	Q9W7R0 gallus gall
10	41	77.4	2133	2 Q813V5 PLAF7	O813V5 plasmodium
11	40	75.5	186	2 Q7NBA0 MYCGA	O7NBA0 mycoplasma
12	40	75.5	548	2 Q62019 CABEL	O62019 caenorhabdi
13	40	75.5	575	2 Q4P6K3 USTWA	Q4P6K3 usitilago ma
14	39	73.6	339	1 PER29 ARATH	Q91SP0 arabidopsis
15	39	73.6	877	2 Q7RGA6 PLAYO	Q7RGA6 plasmodium
16	39	73.6	940	2 Q4Z453 PLABE	Q4Z453 plasmodium
17	38	71.7	118	1 Y849 HELPJ	Q9ZJ99 helicobacte
18	38	71.7	196	2 Q4HN72 CAMLA	Q4HN72 campylobact
19	38	71.7	282	2 Q9CG16 LACLA	Q9CG16 lactococcus
20	38	71.7	283	2 Q8DZT4 STRA5	Q8DZT4 streptococc
21	38	71.7	283	2 Q8E511 STRA3	Q8E511 streptococc
22	38	71.7	284	2 Q5M022 STRT1	Q5M022 streptococc
23	38	71.7	284	2 Q5M4N7 STRT2	Q5M4N7 streptococc
24	38	71.7	331	2 Q5KD08 CRYNE	Q5KD08 cryptococcu
25	38	71.7	333	2 Q55PK8 CRYNE	Q55PK8 cryptococcu
26	38	71.7	519	2 Q72M60 LEPIC	Q72M60 leptospira
27	38	71.7	519	2 Q8EYN9 LEPIN	Q8EYN9 leptospira
28	38	71.7	829	2 Q4Z5E3 PLABE	Q4Z5E3 plasmodium
29	38	71.7	953	2 Q4Y0L8 PLACH	Q4Y0L8 plasmodium
30	37	69.8	86	2 Q7YRW0 SHEEP	Q7YRW0 ovis aries
31	37	69.8	104	2 Q5WDR3 BACSK	Q5WDR3 bacillus cl

32	37	69.8	174	2 Q7RNI9 PLAYO	Q7RNI9 plasmodium
33	37	69.8	338	2 Q626B2 CAEBR	Q626B2 caenorhabdi
34	37	69.8	499	2 Q4RVL5 TETNG	Q4RVL5 tetraodon n
35	37	69.8	520	2 Q5FVY8 ORISA	Q5FVY8 oryza sativ
36	37	69.8	590	2 Q57Y41 9TRYP	Q57Y41 trypanosoma
37	37	69.8	636	2 Q55FG4 DICDI	Q55FG4 dictyosteli
38	37	69.8	639	2 Q797B3 BACSU	Q797B3 bacillus su
39	37	69.8	639	2 Q65D92 BACLD	Q65D92 bacillus li
40	37	69.8	653	2 Q06487 BACSU	Q06487 bacillus su
41	37	69.8	677	2 Q7RE75 PLAYO	Q7RE75 plasmodium
42	37	69.8	1437	2 Q7YIG8 CRYPV	Q7YIG8 cryptospori
43	37	69.8	1475	2 Q5CLD0 CRYHO	Q5CLD0 cryptospori
44	37	69.8	1476	2 Q5CX72 CRYPV	Q5CX72 cryptospori
45	36	67.9	50	2 Q4SEW0 TETNG	Q4SEW0 tetraodon n

ALIGNMENTS

RESULT 1
Q90WY7_COTJA
ID Q90WY7_COTJA PRELIMINARY; PRT; 71 AA.
AC Q90WY7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Agouti-related protein (Fragment).
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Coturnix.
OX NCBI_TaxID=93934;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Hypothalamus.
RA MEDLINE=22003442; PubMed=12008019; DOI=10.1016/S0169-328X(02)00145-6;
RX Boswell T., Li Q., Takeuchi S.;
RT "Neurons expressing neuropeptide Y mRNA in the infundibular
RT hypothalamus of Japanese quail are activated by fasting and co-express
RT agouti-related protein mRNA."
RL Brain Res. Mol. Brain Res. 100:31-42(2002).
DR EMBL; AY048849; AAL06600.1; -; mRNA.
DR HSSP; O00253; 1MR0.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009755; P:hormone-mediated signaling; IEA.
DR InterPro; IPR007733; Agouti.
DR Pfam; PF05039; Agouti; 1.
FT NON TER 1
SQ SEQUENCE 71 AA; 7866 MW; BEF043C9E7A71B22 CRC64;
Query Match 79.2%; Score 42; DB 2; Length 71;
Best Local Similarity 80.0%; Pred. No. 2.5; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 2;

Qy 1 YDRFFNAPFY 10
| | | | |
Db 49 YCRFFNAPFY 58

RESULT 2
Q6J648_SHEEP
ID Q6J648_SHEEP PRELIMINARY; PRT; 105 AA.
AC Q6J648;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Agouti-related peptide (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]

```

RP NUCLEOTIDE SEQUENCE.
RA Wagner C.G., McMahon C.D., Marks D.L.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY596306; AAT41659.1; -; Genomic_DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009755; P:hormone-mediated signaling; IEA.
DR InterPro; IPR007733; Agouti.
DR Pfam; PF05039; Agouti; 1.
FT NON_TER 1
FT NON_TER 105
FT NON_TER 105
SQ SEQUENCE 105 AA; 11665 MW; EP54258B2EDB1461 CRC64;

Query Match 79.2%; Score 42; DB 2; Length 105;
Best Local Similarity 80.0%; Pred. No. 3.8;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YDRFFNAFY 10
Db 88 YCRFFNAFY 97

RESULT 3
Q9GLM5_PIG
ID Q9GLM5_PIG PRELIMINARY; PRT; 121 AA.
AC Q9GLM5
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Agouti-related protein (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Hypothalamus;
RA Matteri R.L., Dyer C.J.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220531; AAG09464.1; -; mRNA.
DR HSSP; O00253; 1HYK.
DR SMR; Q9GLM5; 76-121.
DR GO; GO:0009755; C:extracellular region; IEA.
DR GO; GO:0005576; C:hormone-mediated signaling; IEA.
DR InterPro; IPR007733; Agouti.
DR Pfam; PF05039; Agouti; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 121 AA; 13276 MW; DD736F01B5B5766E CRC64;

Query Match 79.2%; Score 42; DB 2; Length 121;
Best Local Similarity 80.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YDRFFNAFY 10
Db 98 YCRFFNAFY 107

RESULT 4
AGRP_MOUSE
ID AGRP_MOUSE STANDARD; PRT; 131 AA.
AC P56473; O35967;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Agouti-related protein precursor.
GN Name=AgRP; Synonyms=AgRP, Art;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129;
RX MEDLINE=97458244; PubMed=9311920; DOI=10.1126/science.278.5335.135;
RA Ollmann M.M., Wilson B.D., Yang Y.K., Kerns J.A., Chen Y., Gantz I.,
RA Barsh G.S.;
RT "Antagonism of central melanocortin receptors in vitro and in vivo by
agouti-related protein.";
RL Science 278:135-138(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97230362; PubMed=9119224;
RA Shutter J.R., Graham M., Kinsey A.C., Scully S., Luethy R.,
RA Stark K.L.;
RT "Hypothalamic expression of ART, a novel gene related to agouti, is
up-regulated in obese and diabetic mutant mice.";
RL Genes Dev. 11:593-602(1997).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6; Tissue=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Skalska U., Smallos D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Plays a role in weight homeostasis. May play a role in
the regulation of melanocortin receptors within the hypothalamus
and adrenal gland, and therefore in the central control of
feeding.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in arcuate nucleus and median
eminence, adrenal gland (medulla), hypothalamus, testis, and lung.
CC -!- INDUCTION: Hypothalamic expression is elevated circa 10-fold in
ob/ob and db/db mice.
CC -!- SIMILARITY: Belongs to the agouti family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC
CC EMBL; U89484; AAB68620.1; -; mRNA.
CC EMBL; U89486; AAB68622.1; -; Genomic_DNA.
CC EMBL; BC079902; AAT79902.1; -; mRNA.
CC HSSP; O00253; 1MR0.
CC SMR; P56473; 86-131.
CC Ensembl; ENSMUSG00000005705; Mus musculus.
CC MGI; MGI:892013; AgRP.
CC GO; GO:0005615; C:extracellular space; TAS.
CC GO; GO:0005184; F:neuropeptide hormone activity; IEA.
CC GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
CC GO; GO:0007582; P:physiological process; IEA.
CC InterPro; IPR007733; Agouti.
CC Pfam; PF05039; Agouti; 1.
KW Signal.
FT CHAIN 21 131 Agouti-related protein.
FT SIGNAL 1 20 Potential.

```